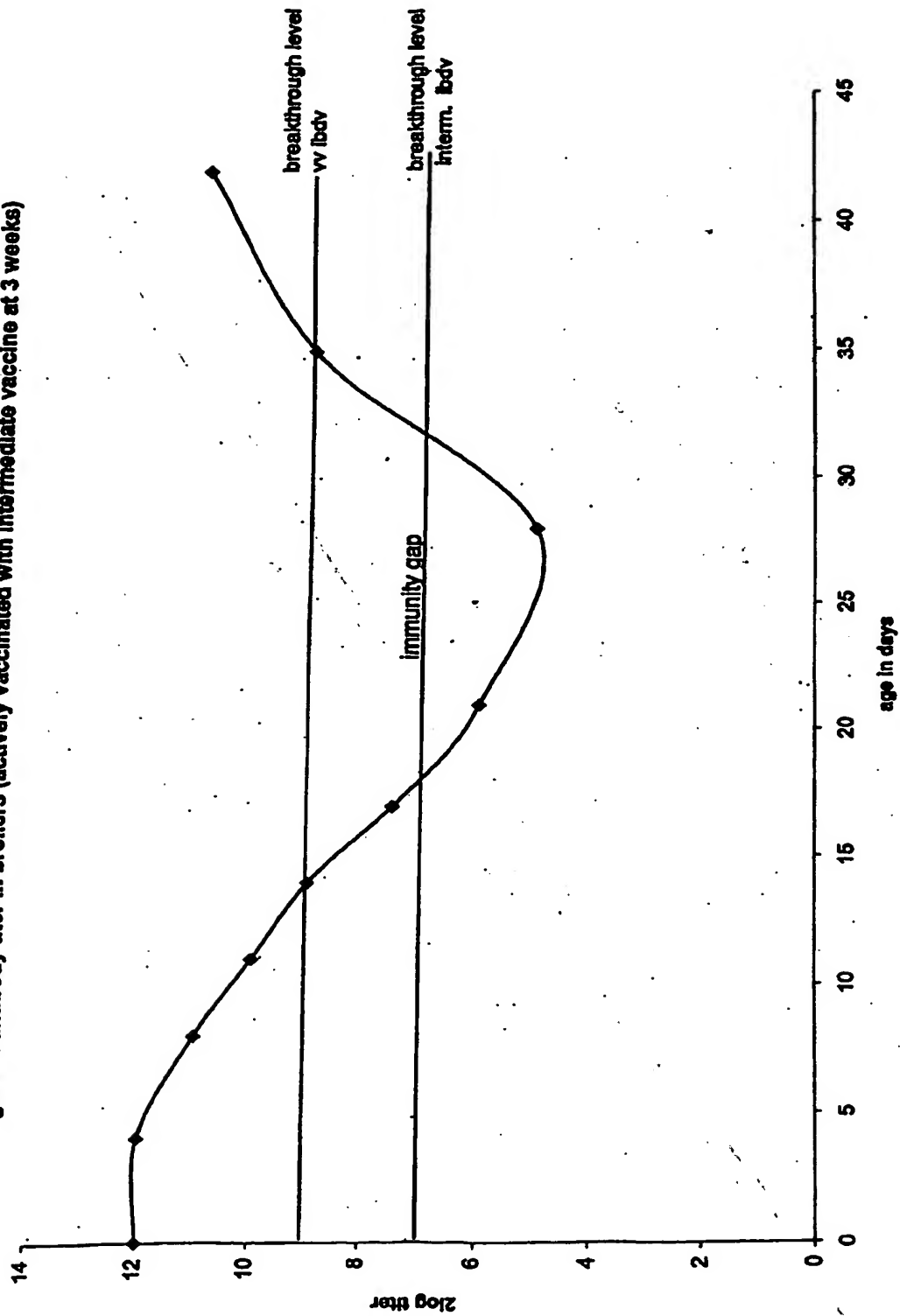


#5

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Figure 1: antibody titer in broilers (actively vaccinated with intermediate vaccine at 3 weeks)



TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

Inventor: Boot et al.
Serial No.: 10/046,671
Docket No.: 2183-5238US

10046671.050602

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Fig.2a Alignment of IBDV A-segment cDNA sequences

Consensus	GGATGAGATC GGTCTGACCC GGGGGGATC ACCCGGGGAC AGGCTGACAA GGTCTGTGTC CAGATGAGAA CTGCT	75
CEP94-AC.T... ..T.....	75
D6948-AT.A... ..C.....	75
TY89-A	
Consensus	CCTCTACAA TGTATCATTT GATGTTTATG AGAGATCAGA CAAACATGTC CAGCGTGCAC BACCTGCAAA GATCA	150
CEP94-AC..... ..C..... ..A.....	150
D6948-AT..... ..T..... ..G.....	150
TY89-A	
Consensus	AACCAACAGC ATTGTTCCTT TCATACGAGG CCTCTGTATG CCACCAACGC GACCGGGGTC CATTCGGGAC GACAC	225
CEP94-A	225
D6948-A	225
TY89-A	
Consensus	CCTTAGAGAG CACACTCTCA GGTCTGAGAC CTCGACCTAC AATTGACTG TGGGGGACAC AGGCTCAGGC CTAAAT	300
CEP94-A	...G.....	300
D6948-A	...A.....	300
TY89-A	
Consensus	TGTCTTTTTC CTTGGTTTCC CTGCTCAAT TGTGGGTGCT CACTACACAC TGCAGAGCAA TGGGAACATC AAGTT	375
CEP94-AA.....	375
D6948-AT.....	375
TY89-A	
Consensus	CGATCAGATG CTCTGACTG CCAGAACCT ACCCGCCATG TACACTACT GCAGGCTAGT GATCGGATG CTCAC	450
CEP94-AT.....	450
D6948-AC.....	450
TY89-A	
Consensus	AGTGAAGTCA AGCAGCTTC CTGGTGGCGT TTAGCACA TAAGGACCA TAAGGCGCT GAGCTTCCAA GGAAG	525
CEP94-AT..... ..C.....	525
D6948-AC..... ..T.....	525
TY89-A	
Consensus	CCTGATGAAA CTGACGATG TTAGCTACAA TGGGTGATG TCTGCAACG CCAACATCAA GGCAGAAATY GGGAA	600
CEP94-A	600
D6948-A	600
TY89-A	
Consensus	GGTCTGATA GGGGAGGGG TTAGCGTCT CAGCTTACCC ACATCATAG ATCTTGAGTA TGTGAGCTY GGTGA	675
CEP94-AC..... ..G..T.....	675
D6948-AA..... ..A..C.....	675
TY89-A	
Consensus	GGCATTCGC GGTATGGGC TTGACCCAAA AATGGTAGCC ACATGTGACA GCGTGACAG GCGCGGATC TACAC	750
CEP94-AA..... ..T..... ..C.....	750
D6948-AT..... ..C..... ..A.....	750
TY89-A	
Consensus	CATACTUCA GCGATGATF ACCAATCTC ATCACATGAC CAACAGGTC GGTATACAT CACTCTTTC TCAGC	825
CEP94-A	825
D6948-A	825
TY89-A	
Consensus	TAATATGAT GGCATACAA GCTCAGCTT YGGGGAGAG CTGTGTTTC AAACAAGGCT CCAGGCGCTT RTACT	900
CEP94-A	C..C..T... ..G..T..... ..G.....	900
D6948-A	T..T..C... ..A..C..... ..A.....	900
TY89-A	
Consensus	GGGTGCTACC ATCTACTTA TAGGCTTGA TGGGACGGC GTAATACCA GAGCTGTGC CCACACATG GGGCT	975
CEP94-A	...C..C... ..C..... ..A.....	975
D6948-A	...T..T... ..T..... ..T.....	975
TY89-A	

TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Consensus	RACACCGCC ACTGACAMCC TTWTGCCATT CAATTTGTGT ATTCCAMCA ROAGATAMC CAGGCCATC ACATC	1050
CEP94-A	G...A.... ..C..... ..F..... ..C..... ..A..... ..A..... ..G..... ..G.....	1050
D6948-A	A...G.... ..T..... ..A..... ..A..... ..C..... ..G..... ..G..... ..G.....	1050
TT89-A	
Consensus	CATCAACTG GAGATAGTG CCTCAAAAG TGTGTGTCTG GCGGGGGTC AGATGTCGTG GTCTGCAAGW GGGAG	1125
CEP94-AA..... ..G..... ..G..... ..A.....	1125
D6948-AG..... ..A..... ..A..... ..T.....	1125
TT89-A	
Consensus	CCTACCATG AGATCCATG GTGCCACTA TCCAGGGCC CTGGGTCCCG TCACCTCATG AGCTACGAA AGAGT	1200
CEP94-AT..... ..C..... ..G..... ..G..... ..A.....	1200
D6948-AC..... ..A..... ..A..... ..A.....	1200
TT89-A	
Consensus	GCCACAGGA TCTGTCTTA CGGTGCTGTG GTTGACACAC TTCAGCTGA TCCCAATCC TGAATGACA AAGAA	1275
CEP94-AC..... ..T.....	1275
D6948-AT..... ..C.....	1275
TT89-A	
Consensus	CCTGTTACA GAATACGCC GATTGCCC AGAGCCATG AACTACCAA AATTGATCT GATGAGAGG GAGCG	1350
CEP94-AT..... ..C.....	1350
D6948-AC.....	1350
TT89-A	
Consensus	TCTTGATC AGAGCCCTT GCCACAGAG GAGTACACT GACTTGTGT ARTACTTCT GAGGTGCCC GACT	1425
CEP94-AC..... ..T..... ..A.....	1425
D6948-AA..... ..C..... ..G.....	1425
TT89-A	
Consensus	CAACTCTCC CTGAGATTG CAGGACATT YGCTTCAA GACATATCC GGGCCGAG GAGATAGCT GTGCC	1500
CEP94-AC..... ..A..... ..A.....	1500
D6948-AT..... ..C.....	1500
TT89-A	
Consensus	GTTGTCTCT ACATTTTCC CACTGCCC TCCCTAGCC CATGCATTG GGGAGGTGT AGACTACTG CTGGG	1575
CEP94-AC..... ..T..... ..T.....	1575
D6948-AT..... ..C..... ..C.....	1575
TT89-A	
Consensus	CGATGAGCA CAGGCTCTT CAGGACTGC TGAAGCCCG TCAAGAAAG CAGGACTGC CTCAGGCCC ATAGG	1650
CEP94-A	1650
D6948-A	1650
TT89-A	
Consensus	GCACTACT CTGCCCCC ACAGGGGTA GAGGTATC GGAATCTT TTCAAGTCC CAGGATCTT GTAGT	1725
CEP94-AG..... ..A..... ..C..... ..C.....	1725
D6948-AA..... ..G..... ..T.....	1725
TT89-A	
Consensus	CGACGGATT CTTCCTTAC CTGGTACT CCGGGTCA CACAACTCG ACTGCTT TACAGAGGT GGCAC	1800
CEP94-AT..... ..G..... ..T..... ..A.....	1800
D6948-AC..... ..A..... ..C..... ..G.....	1800
TT89-A	
Consensus	GCTATTCCCT GTGGTATTA GCACATGGA AGATGCCATG ACACCCAAAG CATTGACAG CAAATATTT GCTGT	1875
CEP94-AT..... ..T..... ..C..... ..T.....	1875
D6948-AC..... ..C..... ..T..... ..C.....	1875
TT89-A	
Consensus	CATTGAGCC GTGCGAGAG ATCTCCACC TCGTCTCAA AGAGATCTT TCAAGACAC TCTCTCTGA CAZAG	1950
CEP94-AC..... ..T..... ..A..... ..T..... ..C.....	1950
D6948-AT..... ..A..... ..C..... ..T.....	1950
TT89-A	

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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Consensus	AGTCTATGGA TATCTCTCAG ATGGGTTACT TCCACTGGAG ACTGGGAGAG ATTACACCOF KUTCCCAATA GATGA	2023
CEP94-AC..... T.....	2023
D6948-AT..... G.....	2023
TY89-A	
Consensus	TGTCTGGAC GACAGCATTG TGTCTCTCA AGATCCCAAT CCTCTATTG TGGGAACAG TGGAAATCTA GGCAT	2100
CEP94-AT.....	2100
D6948-AC.....	2100
TY89-A	
Consensus	AGCTACATG GATGTGTTT CACCCAAAT CCGATACAT GTGGCTATGA CCGGAGCOCT CAATGCTTCT GCGA	2175
CEP94-AA..... ..T..... ..T..T.G.	2175
D6948-AC..... ..C..... ..C..C.A.	2175
TY89-A	
Consensus	GATTGAGAA GTAGCTTTA GAGCACCAG CTCGCCACT GCACACGAC TTGGCTTAA GTTGGCTGAT CCGG	2250
CEP94-AA..A..... ..T.....	2250
D6948-AC..G..... ..C.....	2250
TY89-A	
Consensus	GGCATTGAT GTTACACCG GTTCTACTG GGCACGCTT ATCAACCTT TTCTCTCAA TCCGCGGAC TGGG	2325
CEP94-A	A....C..T..A..... ..C..... ..A....C	2325
D6948-A	T....T..C..G..... ..T..... ..G....T	2325
TY89-A	29
Consensus	CAGGTTCCY TACTCAAC TCCCTATCT TCCACGAGG GCGGACCTC AGTMCATCT KGCCTGCGG GCCTC	2400
CEP94-A	...C..C..CA..A..C.. T....C..AT ..A....C ...A.C.C.. T...A...T..A..	2400
D6948-A	...C..C..TT..A..C.. T....C..AT ..A....C ...A.G.C.. G...A...C..T..	2400
TY89-A	...T..A..CT..C..T.. C....A..CA ..T....T ...T.C.T.. G...C...A..C..	104
Consensus	GGATTCGAA GAGACCCCG AACTGAGG TCTGTGAGG GCGATGAGG CCGGCGGCA GGTGGAGCCA TTCT	2475
CEP94-A	A..... ..C..... GAG T..C..CA..A ..A....A ..A..A..C.. ..G..... C..A..	2475
D6948-A	A..... ..C..... GAG C..C..CA..A ..C....A ..A..A..C.. ..G..... C..G..	2475
TY89-A	C..... ..A..... AGA C..T..GC..T ..A....C ..T..T..A.. ..C..... T..G..	179
Consensus	CCCTGCGC CTGCTGCT TCTGTGCTT GAGAGGAA GCGATGCTA CTGATGCTG TACTTGGG CTCAG	2550
CEP94-A	..AA..T..A ...AGT..G.C.....G..TG..T.....C.....A.....	2550
D6948-A	..AA..T..G ...AGC..G.C.....G..TG..T.....C.....A.....	2550
TY89-A	..GC..A..T ...CAG..C.T.....A..CA..C.....T.....C.....	254
Consensus	CGACCCGAC GCGATGGA TGGGATTT TCTGCGAA GCGGCGGAG CCGGCGGCA GTCCGAGAG GCCA	2625
CEP94-AC..TC... ..CGA... T..T....C ..A..A..A..A..A..C..... ..A..G.....	2625
D6948-AC..TC... ..CGC... T..C....C ..A..A..A..A..A..C..... ..A..A.....	2625
TY89-AA..CA... ..AAA... C..A....T ..T..C..G..C..A..... ..G..G.....	329
Consensus	GTATGGACR GCGGCTACG GATGCGGCT TGGGCGCTT ACCTCGGAG AGCAGACAG GAGAAAGAC ACAG	2700
CEP94-A	...C..G..A ..A..... TC.G..... ..A....G..A..... ..A.....	2700
D6948-A	...C..G..A ..A..... CC.G..... ..T....G..A..... ..A.....	2700
TY89-A	...T..C..G ..T..... TA.A..... ..G....A..G..... ..G.....	404
Consensus	GATCTGAG AGATGAGA CBTGGGCT CTACTTCA ACACCGAAT GGTAGCACT CAATGGGAC CGG	2775
CEP94-AA... ..G..C..... ..T..... ..A..... ..T..... ..A.....	2775
D6948-AA... ..G..T..... ..T..... ..A..... ..T..... ..G.....	2775
TY89-AC... ..A..G..... ..C..... ..G..... ..C..... ..A.....	479
Consensus	GGCAGCCCG GCGGCTTCA AGTACTGCA AACACGAG GAGATACCG AGCGGAGCA GAGTATCTA GACTA	2850
CEP94-A	G..... ..A..... G.....C.. ..G....G..C..A..... ..T..T.....	2850
D6948-A	G..... ..A..... G.....C.. ..T....T..T..A..... ..C..T.....	2850
TY89-A	C..... ..C..... A.....A.. ..A....A..A..C..... ..C..C.....	554
Consensus	TGTGATGCA GAGAGAGCC GGTGGGCTC AGAGAGAC RTCTTAAAG CAGTACCTC GATCTGAGG GCTC	2925
CEP94-A	C....T..AA.....A..A..C..... ..T.....	2925
D6948-A	C....T..AA.....A..A..C..... ..T.....	2925
TY89-A	T....C..GG.....G..T..... ..C.....	629

TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

Inventor: Boot et al.
Serial No.: 10/046,671
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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Consensus	AGGACAGGCG GAGCCACCCC AACCTTTCAT AGACGAGGT OCCAAGTCT ATGAATCAA CAGTGGGCT GGTCC	3000
CEP94-AA ..G..... ..T..... ..T....AA..... ..A... ..C..	3000
D6948-AA ..G..... ..C..... ..C....AA..... ..G... ..C..	3000
TY89-AT ..A..... ..C..... ..C....GG..... ..G... ..T..	784
Consensus	HAACCAAGAG CAGATGAAG ATCTGCTCT GACTGGGATG GAGATGAGC ATGCAATCC CAGCGGGCT CTAC	3075
CEP94-A	A.....A..AA. .T.....T.T...	3075
D6948-A	C.....A..AA. .T.....C.C...	3075
TY89-A	A.....G..GG. .C.....C.C...	779
Consensus	AAAGCCGAG CCAAAACCCA ATGCTCCMC ACAGAGACCC CCGGCGGCG TGGGCGGCTG GATCAGGCG GTCTC	3150
CEP94-AC... ..A..... ..T..... ..A.C	3150
D6948-AC... ..A..... ..T..... ..G.T	3150
TY89-AA... ..T..... ..A..... ..A.G	854
Consensus	TGATGAGAC YTGAGTGAG GYNCTGGGA GTCTCCGGAC ACCACCCCG CAGGTGTGA CACCACTTA KMETT	3225
CEP94-A	...T..... C.T..... .TA..... ..T..... ..CG GACT.	3225
D6948-A	...T..... C.T..... .CT..... ..C..... ..CG GCCA.	3225
TY89-A	...C..... T.G..... .CT..... ..T..... ..AA TCAC.	929
Consensus	ASMGATTC AAATTGATC CATTGCGGG TCCCC	3260
CEP94-A	.CAAC..C.C	3260
D6948-A	.CAAC..C.C	3260
TY89-A	.GTGA..T.G	964

TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINESInventor: Boot et al.
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Fig.2b		Alignment of IBV B-segment cDNA sequences	
Consensus	GGATACGAG GGTCTGACC TCTGGATCT AGGAATAC GTGGCTACA GGGGTGATG CCGCGCTGG CTGCC	75	
CEP94-BC...AA..G.....G.....	75	
D6948-BT...GC..A.....A.....	75	
Consensus	ACGTTATGG CTCTCTCTCT TGTAGATCT ECGACCATGA GTGACTTTT CAATAGTCA CAGGCGGAA GCAGG	150	
CEP94-BG.....A.....C.....C.....	150	
D6948-BA.....G.....T.....A.....	150	
Consensus	ATHTCAGCG GTTCGGCAT AAGGCTACG OCTGGACAG ATGTGGAGA ACTCTGATC CCTAAGTTT GGTGT	225	
CEP94-B	..C.....T.....A..C.....T.....A..T.....	225	
D6948-B	..A.....A.....G..T.....C.....G..C.....	225	
Consensus	CCAGCTGAG ATCCTTTCG CAGCCTAGT CAGCTGGCA AGTCTCTCG EGAAGAGGC TACAGATTT TCGAG	300	
CEP94-BGC.T.....A.....A.....A..G.....AG..T.....	300	
D6948-BCT.G.....T.....G..A.....G..A.....GA..C.....	300	
Consensus	CCAGCTCTC TACCTGAGA TTAGGATAT GAGCGGATC AATATCTCC WAGCTGAGW TGGTGGGRC AGATA	375	
CEP94-BG..C.....T.....C.....A..T...A.....C..A.....	375	
D6948-BA..T.....T.....T.....T...C...T.....A..G.....	375	
Consensus	GAGGGGCTG TTATAAACG NACTTACTT CTCCATATG GAGATCAGA GTACTTCCG AAGTACTAC CAGCA	450	
CEP94-B	..A..G....C..T.....T.....T.....A..G.....A.....	450	
D6948-B	..G..A....A..C.....C.....C.....T.....A.....	450	
Consensus	CATCGGCCA GCAGGAGAA GCGCATGCG TACCGGCGG AYATGCAAT ACTCAGCAG AGTATTTACT TGTTT	525	
CEP94-B	..T...T....G....C.....C.....C.....T...C.....	525	
D6948-B	..C...G....A....C.....C..T...T.....C..T.....	525	
Consensus	CTCCAGGTC CAGAGGCCA NAGAGGCTW AAGATGAG TACCTTTT RACCCAAAC ATWAGGAYA ARGCC	600	
CEP94-B	..A...A..C...GG...A..G....A..A....CT..G.....A..G..C..G...	600	
D6948-BC.....C..A..TA..T..A....G..C....AC..A.....T..A..T..A...	600	
Consensus	TATGAGATG GAGCTACAT GAGACAGCG ACTGACTTG TGTCTATGA EAGGTTTCC ACTGAGAG ACCCA	675	
CEP94-B	..T..A....A.....A..A..TC.....G..C....G....C....A.....	675	
D6948-B	..C..G....G....C..CA.....T..T....A....T....G.....	675	
Consensus	AAGAGATTC CTCTAAGCT TGGTACAT TTTGAGGCA TTGCGAGCT ACTTGACAT ACHTACCGG TAGGC	750	
CEP94-BG.....T.....C..G.....AC.....	750	
D6948-BA.....C.....A..C.....TT.....	750	
Consensus	CCACCGGTC AGGATGACA GCGCTGGTA CCACTCACA GGTGCGGTC AAGGATGTC GTTCTGACG GAGAC	825	
CEP94-BG.....A.....C.....A.....A...	825	
D6948-BA.....G.....A.....T.....C...	825	
Consensus	GTGATGCG AMTTTGAGT TGAGATTC CTCCGAAA TCAAGCTCA GTCATCAT GTACTTCCT ATGTW	900	
CEP94-BC..C.....A..T.....A.....A.....A.....	900	
D6948-BG..A....G..C.....G..C.....G..C.....T.....	900	
Consensus	GATGACACA AAGGAGAAC NATTGGSAG ATGATAGTA TTTCAACCA GTTCTTREA GAGCTATCA CAGTC	975	
CEP94-BG..A....C....T..C..A.....CA.....A..A.....	975	
D6948-BA..T....G....C..A..G.....TC.....G..G...	975	
Consensus	YTGAGCAG GTCCAGGAC AAGGCTCA AACAGAGA AGCTCTCG CATGTAGT GACTATGCT ACTTA	1050	
CEP94-B	T.....A.....G....A.....A.....T.....T.....	1050	
D6948-B	C.....G.....A.....G.....G.....C.....C.....	1050	
Consensus	TGATGCGC TTTTGTTC NAGGCTGAG AGGTAGACA AAGTACAT GCTCAGCAG ACCCGACCA TATGG	1125	
CEP94-BC.....A.....A.....T.....G.....	1125	
D6948-BT.....C.....C.....C.....T.....	1125	
Consensus	TCACTCCAT CCGCAACACA CTTATGATC TGTATGATG CTTGGGCGG GATGTGCAAT ACCCGAATA ACOTG	1200	
CEP94-BC.....T...C.....C.....T.....	1200	
D6948-BA.....A.....A.....T.....C.....	1200	

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Fig.2b Contd. Alignment of IBDV B-segment cDNA sequences

Consensus	TTCACATTC	ARGGGTGTCC	RTCTCTTAC	AATTCACCC	GTTTAGAGG	WGGGTTTAC	AGGTCGTGG	AGTGG	1273
CEP94-B	A.....	A.....	..A.....	...C.....	A...T.G...C.....	1273
D6948-BG.....	G.....	..G.....T.....	T...C.A...G.....	1273
Consensus	ATATGCTTC	CGGAGAAC	CAAGCTTTT	GTAATGCGG	ACACATATA	CATTGTTAC	TGACACAGT	GGTAC	1350
CEP94-B	...T...C.	...A.....TC.TG.....C.....	..A.....	1350
D6948-B	...A...T.	...T.....CT.AT.....C.....	1350
Consensus	TCAATGACC	TAGAGAGGG	TGAGGCAAC	TGACACGTC	AACACATCA	AGCCGCGTG	TACTACATC	TTACC	1425
CEP94-BT..C.	A....A...A..C...	1425
D6948-BG..T.	G....C...C..T...	1425
Consensus	AGAGGTGTT	CGATACAGG	TGACCGGAT	TTCAATCAG	CATGGGCGC	CTTTCGATG	AACCTGCCC	CGGCT	1500
CEP94-BG....	..A..C....	C.....A...A.....C.....G...A...	1500
D6948-BA....	..C..T....	T.....C...G.....	1500
Consensus	CTAGTGTGG	ACTCATCTG	TCTGATGAT	AACCTTCAG	TTAGACGTA	TGCTCAGGC	AGTGGGATG	CAGCC	1575
CEP94-BG....G..	C.....A...G..A..	..T....C...C.....	1575
D6948-BT....A..	T.....T...T..G..	..C....A...T.....	1575
Consensus	ACCTTCATC	ACAACCACT	TTTACGACC	CTGCTGCTG	ACCACTGGA	CTTGATGAG	CACCTACGC	CAGAC	1650
CEP94-B	..G.....C..	CT.G....G	..A....T.C.....	GA...G..C..A.	1650
D6948-B	..C.....T..	TC.T....C	..T....A.T.....	AG...A..T..T.	1650
Consensus	AGCAGAGAT	TCAATCAAT	TGAGACAGG	CTGATATCA	ACTTTAAGT	TGAGAGTTC	ATTGATGAT	TTAGG	1725
CEP94-BG....A....A....	..A..T....	...T.....T..C...	1725
D6948-BA....G....A....	..G..C....	...C.....C..T...	1725
Consensus	GGCAAGCTA	GACAGCTTT	CTCTCTGCA	CAGCCAGGT	ACCTGATGG	AGGGGTTGA	CCAGACAAAT	CCAGC	1800
CEP94-BG..T.....G....T..A..T...	1800
D6948-BC..C.....A....C...G...C...	1800
Consensus	CCACTGTTG	AGCTGACCT	ACTGGGTTG	TGCGACATC	ACAGCAAGA	TCTTGGGATC	TATGCGCGG	TGCTT	1875
CEP94-BT.	...T....	..A..G...	..A..T..A.C.....	1875
D6948-BA.	...G....	..C..A...	..T..A..T.T.....	1875
Consensus	GACAGGATC	GCTTATTTT	TTCTGCTGG	TATCCAGAG	GATAGAGAA	TAAGATCTC	AATCCAGAG	TTGGG	1950
CEP94-BC.....	T.....G..	..A.....	C..G..T...	..G....A..C...	1950
D6948-BT.....	C.....A..	..G.....	T..A..C...	..A....G..T...	1950
Consensus	ATGAGGAGG	CATACAGAT	WTCGATAT	GAGGCGTTG	GTTGATAGG	TGTTGAGAC	TACCCACTC	TGAC	2025
CEP94-BG..G..	A.....T	2025
D6948-BA.A.	T.....C	2025
Consensus	AAGCTTCCA	AGATATATC	AGTCTGCT	CGCGGATC	TGAGGCGCA	GGGTTCCCG	CTGATGAGT	TGCTT	2100
CEP94-BC....T..C..	..G..C..C..A.....C.....A	2100
D6948-BT....C..T..	..A..T..A..G.....T.....C	2100
Consensus	GGGAGTGGT	CGAGTTGTC	AGGTTGCGG	GAGCTTTGG	AAGCTTCAA	TATCAGCTG	ACGATACAT	CGAGG	2175
CEP94-BT..C...	A.....T	..G..C...	T.....C.....T..T...	2175
D6948-BA..T...	C.....A	..A..T...	C.....A....C..G...	2175
Consensus	AGCTTGGCG	AACATACAC	AGAGTACCC	CCCAAGCTC	CAATGTCAA	CAGACAGTC	AACATGCGG	GGCTT	2250
CEP94-BA....G....A	G.....G..C..T..G..A..C	2250
D6948-BC....T....G	A.....A..T.C..T..G..A	2250
Consensus	AAGCAGTCA	GCAATGCCCT	CAGACCGGT	CGATATAGA	ATGAGCGCG	ACTGATGGT	CTGCTCTCT	TAGCC	2325
CEP94-BC.....T.....C..G..G....T	2325
D6948-BT.....C.....T..A..A....CC.....	2325
Consensus	ACGCGGAGA	GGGCTTCA	AGATGAGTT	AAGGCGAGG	CAGAGCGGA	GAACTCCAC	AGCTTACG	CGAT	2400
CEP94-B	..A..AA..A.	...T..G..	A..T....TC....	..A..C	2400
D6948-B	..C..CC..C.	...A..A..	G..C....CG....T....	..C..T	2400

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Fig.2b Contd. Alignment of IBV B-segment cDNA sequences

Consensus	GAACCCCGTG CAGACTGGTT TGAAATCTCA GAAACTCTGT CAGACTCTCT GGAGAAAGCC GACATTCACA CCAGG	2473
CE794-B C...A.A... ..T... ..T... ..C....	2473
D6948-B T...C.G... ..C.... ..G.... ..T....	2473
Consensus	GTGCTCTACT CAGACTCTGT GGAAACAGAC GAGCTCTTGT AACCTCTTCA GTCTACTTCH GTTACACTTC CCAGG	2550
CE794-BC.... ..C.... ..A..T.. ..G..T..C ..C....	2550
D6948-BT.... ..T.... ..G..C.. ..A..C..A ..C....	2550
Consensus	TACCCAGAG TYAAGAAACC ACAGACCGCC TCCAAACCCG TTCTGGGCT CCACCTGCC CCAGAGAGG CCACC	2623
CE794-BA. .C..... ..C.... ..C.... ..A....	2623
D6948-BG. .T..... ..C.... ..G.... ..G....	2623
Consensus	GGTGTCCAG CAGCTCTTCT CGAGCAGG ACAGACAGAC CAGTGGGCT GAGCTCTCA ACAGCTCCA AGAAC	2700
CE794-BC..... ..A..... ..C.... ..C....	2700
D6948-BA..... ..G..... ..T.... ..T....	2700
Consensus	GGCTGAAA TGGCCAAAG GCGGCAAGC CAAAGAGAA GCGGCAAYA GCGATGTGG GAGCCTCA AGAG	2773
CE794-BC..... ..G.... ..C.... ..C....	2773
D6948-BA..... ..A.... ..T.... ..T....	2773
Consensus	AGGACATAA TCCAGAGCC GGTATCCCG GCTTGGGCT GCGGGGGGCC CC	2827
CE794-B T..... ..C.... ..C....	2827
D6948-B C..... ..C.... ..C....	2827

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10046671 .050602

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Fig.3a	IBDV polyprotein alignment									
Consensus	HTDLQDQTQQ	IVFFVLESLM	PTTGFASIFD	DYLEKHTLAS	ETSTELATVG	DTGSLIVTF	PGTPOSIVGA	HYELO		75
CEP94-PP		75
D6948-PP		75
TT89-PP		
Consensus	ENGHTFDDM	LLFAGELPAS	HTYCLVRS	LTVRSTTLFG	GVIALNOTIN	AVTPQOSLER	LDVSTIRGLE	SATAN		150
CEP94-PP		150
D6948-PP		150
TT89-PP		
Consensus	IRKIGIVLV	GGVTVLSLP	TSYELQVEL	GVPIPAIGLD	PMVATCDSS	DNRVTTITA	ADDTQFESQY	Q.GGV		225
CEP94-PPP..		225
D6948-PPA..		225
TT89-PP		
Consensus	TYTLPSANID	AITELS.GGE	LWPTSEV.GL	.LGATVYLIG	PDGTAVITRA	VAA.SGZT.S	TEML.PTH.V	IFT.E		300
CEP94-PPV..E..	..V..N...T..L...L..	...N..	300
D6948-PPD...A..M...I..	...S..	300
TT89-PP		
Consensus	ITQPTISIEL	KIVTRESGOQ	AGDQHEHA	GLAVTTHGG	HTFGALRPVT	LVATERVATG	SVTVAGVEN	FELIP		375
CEP94-PP		375
D6948-PP		375
TT89-PP		
Consensus	HTPLAQLVY	HTGFDPGM	HTYELLSER	DALGIKTVWF	TREYDQREY	FMEVAKNSP	LEKNGFQFK	DIDRA		450
CEP94-PP		450
D6948-PP		450
TT89-PP		
Consensus	.KRIAVFVVS	TLFFPAFLA	HAIGGVDTL	LCDEQAQASG	TARAAGKAR	AAGSRIRQLT	LAADKQYEVV	AKLFO		525
CEP94-PP	I.....		525
D6948-PP	L.....		525
TT89-PP		
Consensus	VPQGVVDGI	LASTG.LEGA	HELDVLRG	ATLFTVVITT	VEDANTFKAL	NSKMFVING	VREIQPPSQ	RGEVI		600
CEP94-PP		600
D6948-PP		600
TT89-PP		
Consensus	RTLGGKVTG	YAFQVLSLE	TGRTTVVVI	DDVMDSTEL	SKDPFPTVG	NSGHLAIAM	DVFRKVFVN	VAMTG		675
CEP94-PP		675
D6948-PP		675
TT89-PP		
Consensus	ALGA.GKIR.	VSRSTELAT	AMELGLKLG	SGAFVVTG.	NSGTFIKRFP	NSPDRNSLP	YIALPTLPM	AGRQY		750
CEP94-PP	...C...K		750
D6948-PP	...Y...N		750
TT89-PPT...P		28
Consensus	HLMAASEFK	ETPELEAVR	AMEAANVDP	LPQALSVPN	MLEKGIYTD	KANVALSDSN	AMNSGVLAM	APQAG		825
CEP94-PP		825
D6948-PP	D.....		825
TT89-PP	...L.....	...D...	...D...	...R...Q...K.....		103
Consensus	SKSQAKIYT	AGTQVANGP	TYEAGREK	TRISKHEM	GIYFATPENV	ALSGRNGPSP	QQLKYNMTR	RIKDP		900
CEP94-PP		900
D6948-PP		900
TT89-PPE..		178
Consensus	KEDYLYVHA	SKRLASERQ	ILRANTSTG	APQAEPPQA	FIDEVAKVYE	INSGRPFQSE	QKDLALTAM	SKKIR		975
CEP94-PP		975
D6948-PP		975
TT89-PP	...F.....	V.....R...		253
Consensus	KPRRAPPKK	KPRAPTORP	PGRLGRGRT	VSEKDLK						1012
CEP94-PP	...L...						1012
D6948-PPA...						1012
TT89-PPS...						290

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Fig.3b IBDV VP1 alignment

Consensus	MSD.FEPTQA RS.ISAAPGI EPTAQDVEE LLTPKWVTF EDPLASTPEL AKFLAKENYK .LQFSLPEN EHYET	75
CEP94-VP1	...I..... ..T..... ..V..... ..	75
D6948-VP1	...V..... ..K..... ..I..... ..	75
Consensus	DQILFDLAMI RQIEGAVLKP TISLFDGDS YFPCYTFER PSKIKHAYP FOIALLEQKI YLFLQVPEA. ...LKD	150
CEP94-VP1N EG...	150
D6948-VP1T DM...	150
Consensus	EVTLLQWIR DEATGSGTTH QQATRLVANK EVATGSHPK DPLKLYTPE SIQALLDITL FVQPPQEDCK FAVPL	225
CEP94-VP1	225
D6948-VP1	225
Consensus	TRVPERALV TGVVDG.FEV EDYLPKIKL EGGCLTYGR TQETIGENI AIDKFLREL S.LLKQAOT EENK	300
CEP94-VP1D..... ..T..... ..	300
D6948-VP1E..... ..A..... ..	300
Consensus	KLLKSLDY WYLSGLLFP KARYDKSTW LKTRQWHA PPTPLHLEK ITWFWHSEF NVVLMEQCP ELVYF	375
CEP94-VP1	375
D6948-VP1	375
Consensus	KPTQGLAKI VEMI.AP.EP KALVADNIT IVEHWITSI DLEKHAQCT RQHQAMTY ILTRQWDSG DFWN	450
CEP94-VP1L..E.. ..	450
D6948-VP1M..D.. ..	450
Consensus	QTVATYAKI APALVDEEC LIDELQIKTY QQSGHATY DSHLLSTLV LDQKLM.QP .FQSEFESI ERLG	525
CEP94-VP1E.. E..... ..	525
D6948-VP1K.. S..... ..	525
Consensus	DEPKERSID DIRMELQLV .LAQGYLGG QVEPSQ.SPT VEELLLQWHA TIRKILQITV FVLKELKFC SAATP	600
CEP94-VP1L..... ..S..... ..	600
D6948-VP1F..... ..F..... ..	600
Consensus	KVVEKELKE KVQIEQATV VETELKLVG GMYTFLNKA CQMA.AARR KLEKQFFLD EFLAKSELS EFGHA	675
CEP94-VP1G..... ..	675
D6948-VP1S..... ..	675
Consensus	FQPMKILAV T.EKLAKL. PVPPEPPVM RIVVTOGLEA VEMALTONY KIKAGLSGLV LLATARSLO DAVIA	750
CEP94-VP1S..... ..K..... ..	750
D6948-VP1P..... ..E..... ..	750
Consensus	KAKKILKES KPDQDADMT ERSETLSLL EKADIASKVA REALVETSDA LEAVQSTSVY TIKYFEVMP QTASH	825
CEP94-VP1	825
D6948-VP1	825
Consensus	FVGLKLPK RATOVQALL GAGTSAPKQK EAPTASINAV KAKKQKQK ESQ..	881
CEP94-VP1	881
D6948-VP1	879

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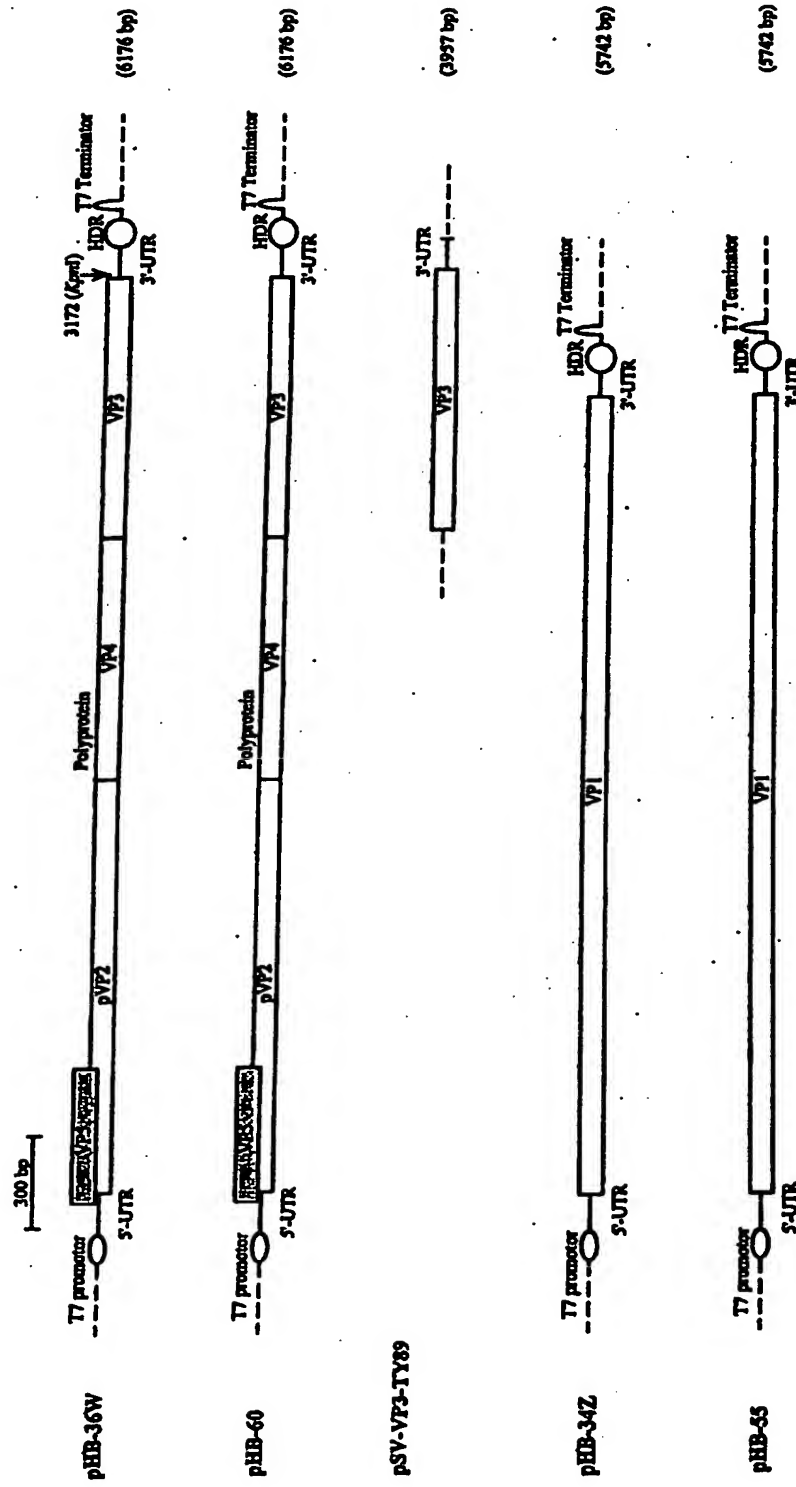
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Fig. 3c IBDV VP5 alignment.

Consensus	MVSRDQTNDR SPD.PARSHP TDCSVHTFES DANKRTGVHS GRNP.EANSQ	50
D6948-VP5R.....R.....	50
CEP94-VP5K.....G.....	50
Consensus	VRDLDLQFDC GGHRVRANCL FFW.FWLANCG CSLHTAEQWE LQVRSDAFDC	100
D6948-VP5F.....	100
CEP94-VP5I.....	100
Consensus	PEPTQQLQLL QASESESSE VIGHT.WWRLC TK.HKKRDL FRKPE	145
D6948-VP5F.....N.....	145
CEP94-VP5S.....R.....	145

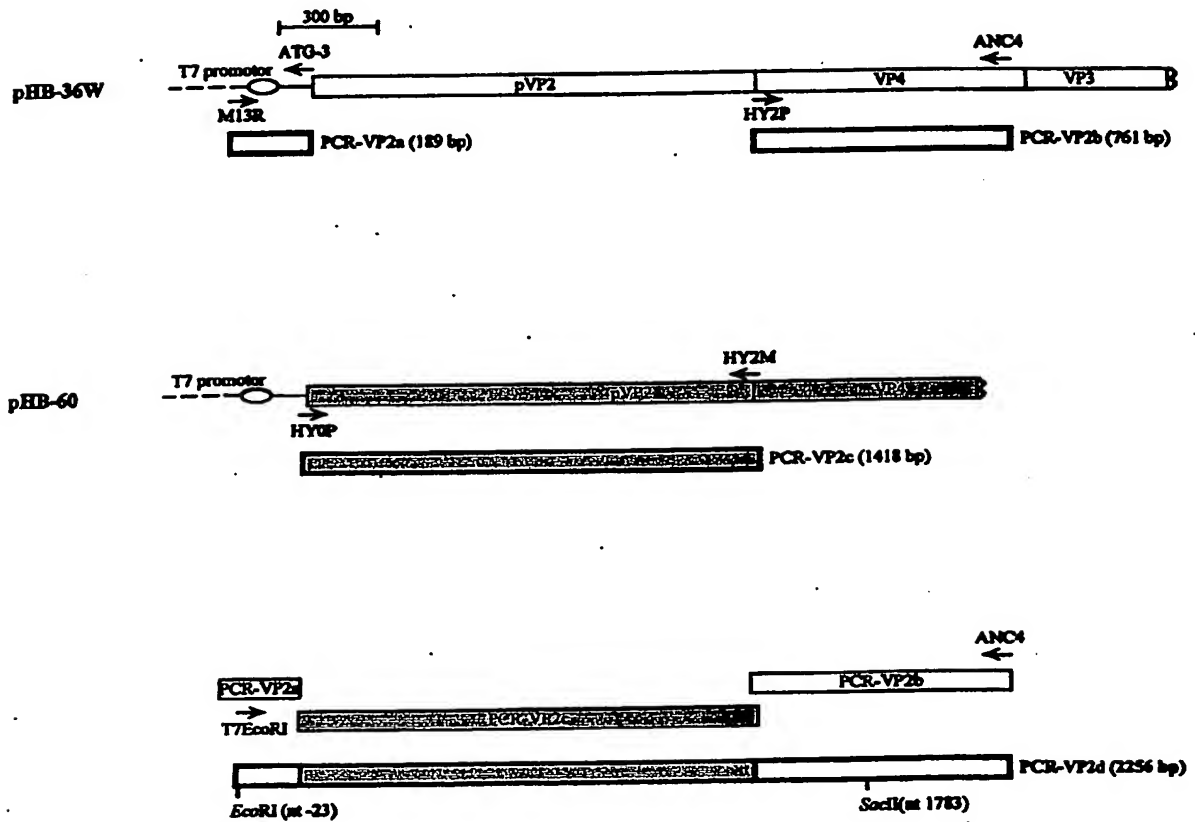
Fig. 4 Schematic representation of the used plasmids



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Fig. 5a

Schematic representation of the construction of PCR fragment PCR-VP2d



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Fig. 5b

Schematic representation of the construction of PCR fragment PCR-VP3c

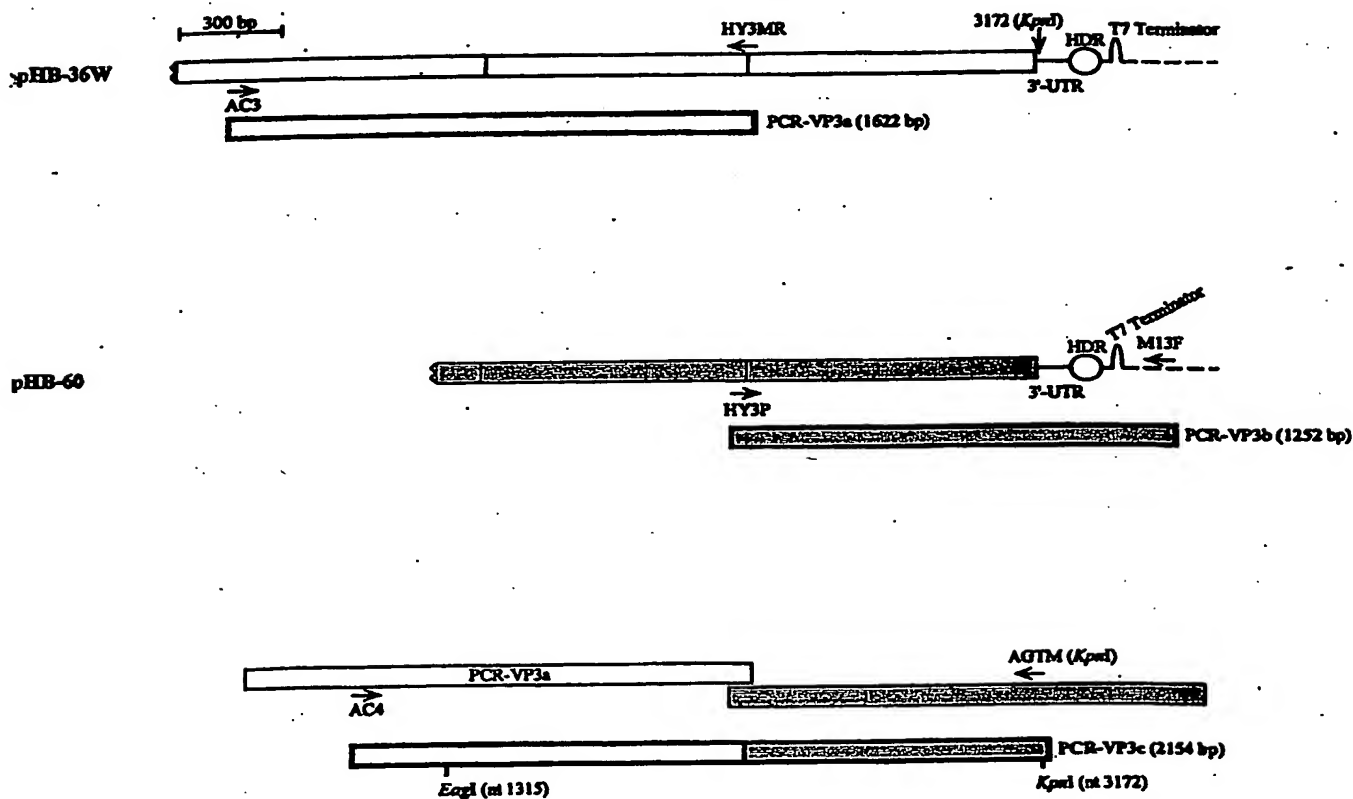
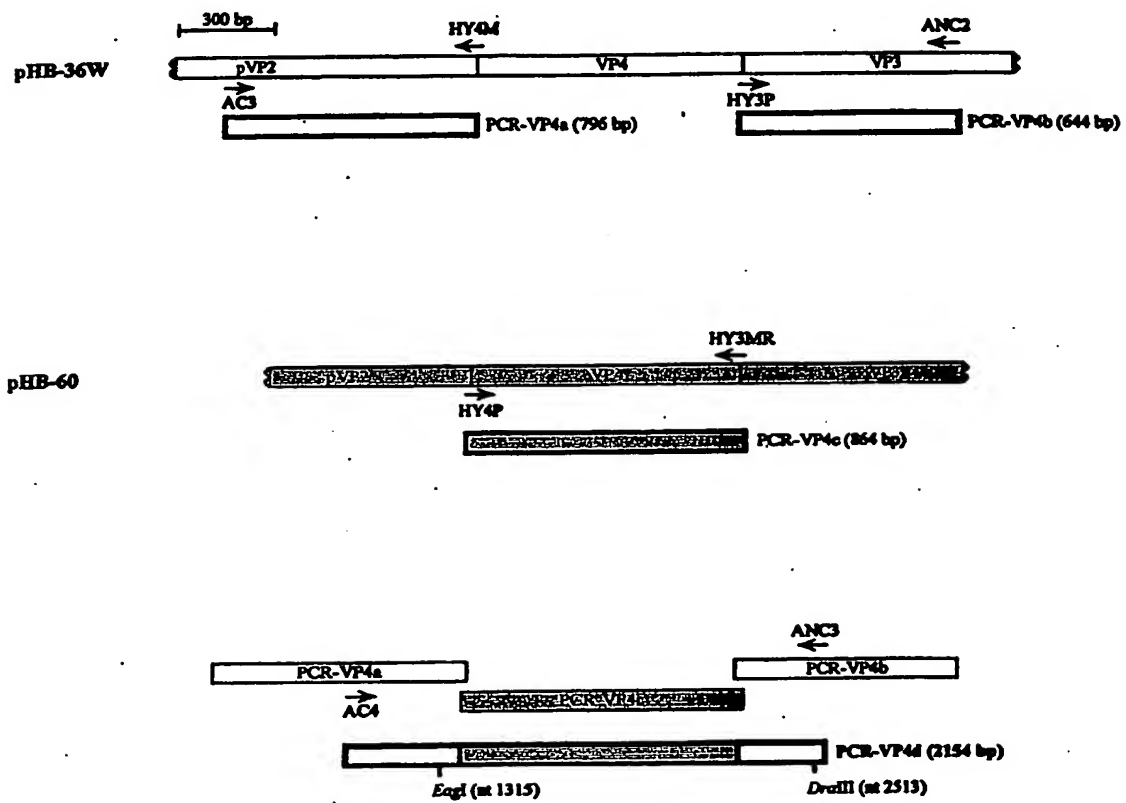


Fig. 5c Schematic representation of the construction of PCR fragment PCR-VP4d



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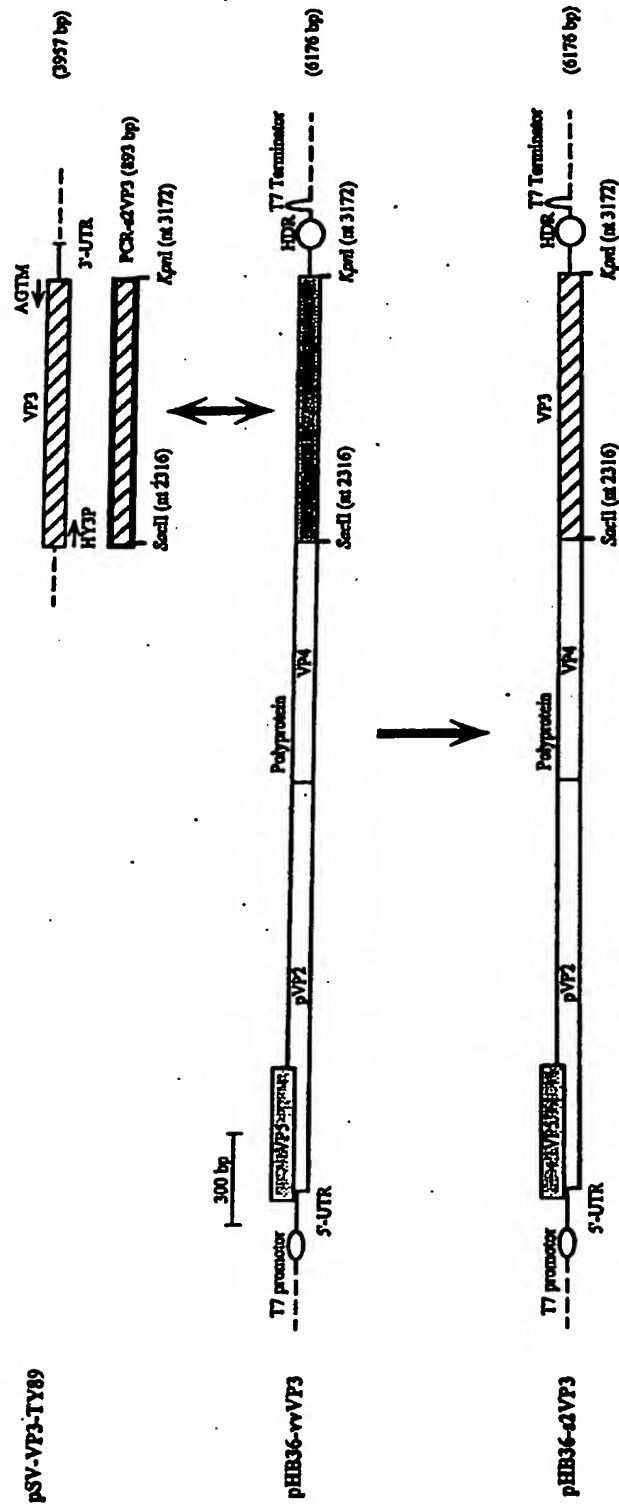
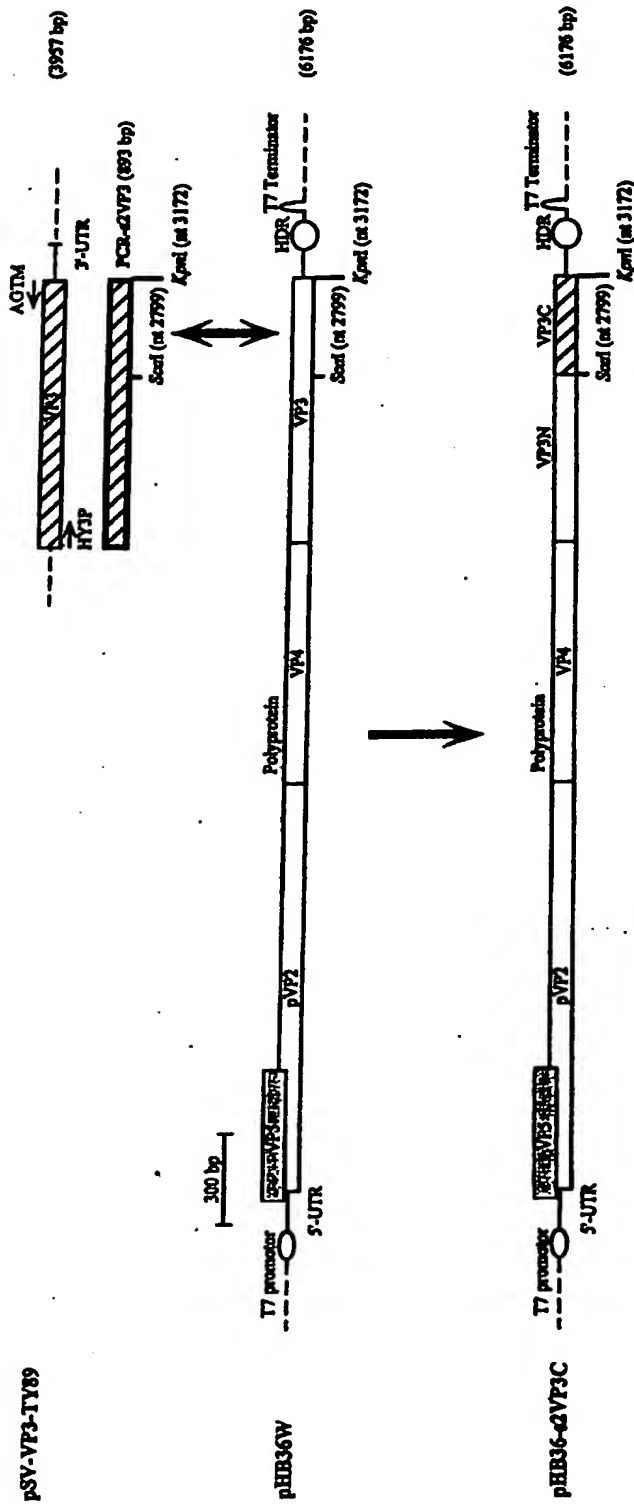
Fig. 5d Schematic representation of the construction of plasmid pHB36-ΔVP3

Fig. 5e. Schematic representation of the construction of plasmid pHR36-2VP3C



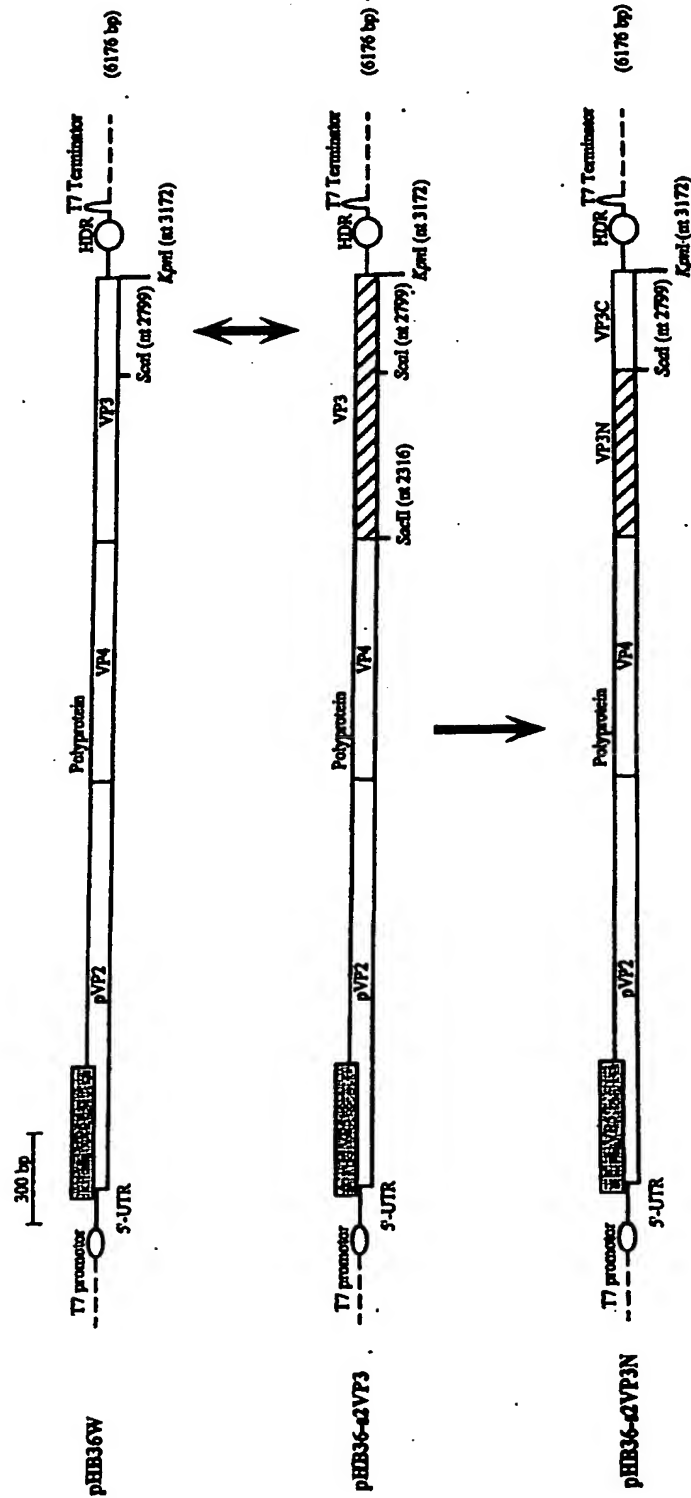
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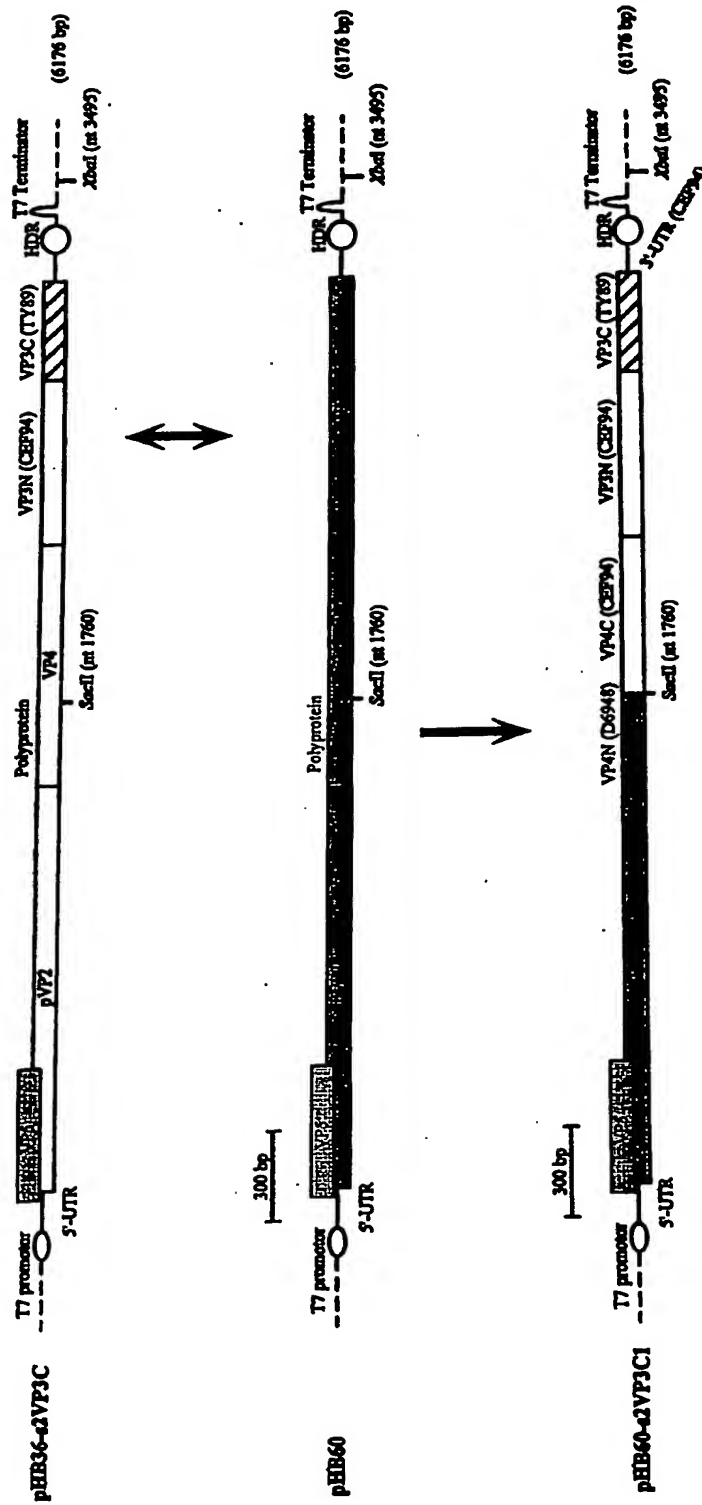
Fig. 5f Schematic representation of the construction of plasmid pHB36- Δ VP3N

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Fig. 5g Schematic representation of the construction of plasmid pHB60- α VP3C1



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Fig. 6

CEP94-PP	724-FPHNPRD	WDRLPYLNL	YLPNAGROY	HLAMAASEFK	ETPELESVR	AMEAANVDP	LFQSALSVFM	WLEENGIVTD	800
TY89-PP	724-.....T.....L.....D.....D.....R...Q...	800
CEP94-PP	MANFALSDPN	AHRMENFLAN	APQAGSKSR	AKYGTAGYGV	EARGPTPEEA	QREKDRISK	KMETMGIYFA	TPREWALNGH	880
TY89-PPK.....	880
CEP94-PP	RGPSGQLKY	WONTREIPDP	NEDYLDYVHA	EKSRLASEEQ	ILRAATSIYG	APQQAEPPOA	FIDEVAKVYE	INHGRGNQOE	960
TY89-PPE.....P.....V.....R.....	960
CEP94-PP	QMKDLLLLTAM	EMKERNPRA	LPKPKPKPNA	PTQRPQRLG	RNIRTVEDED	LE	1012		
TY89-PPP.....S.....	1012		

SacII

VP4 ← VP3

SacI

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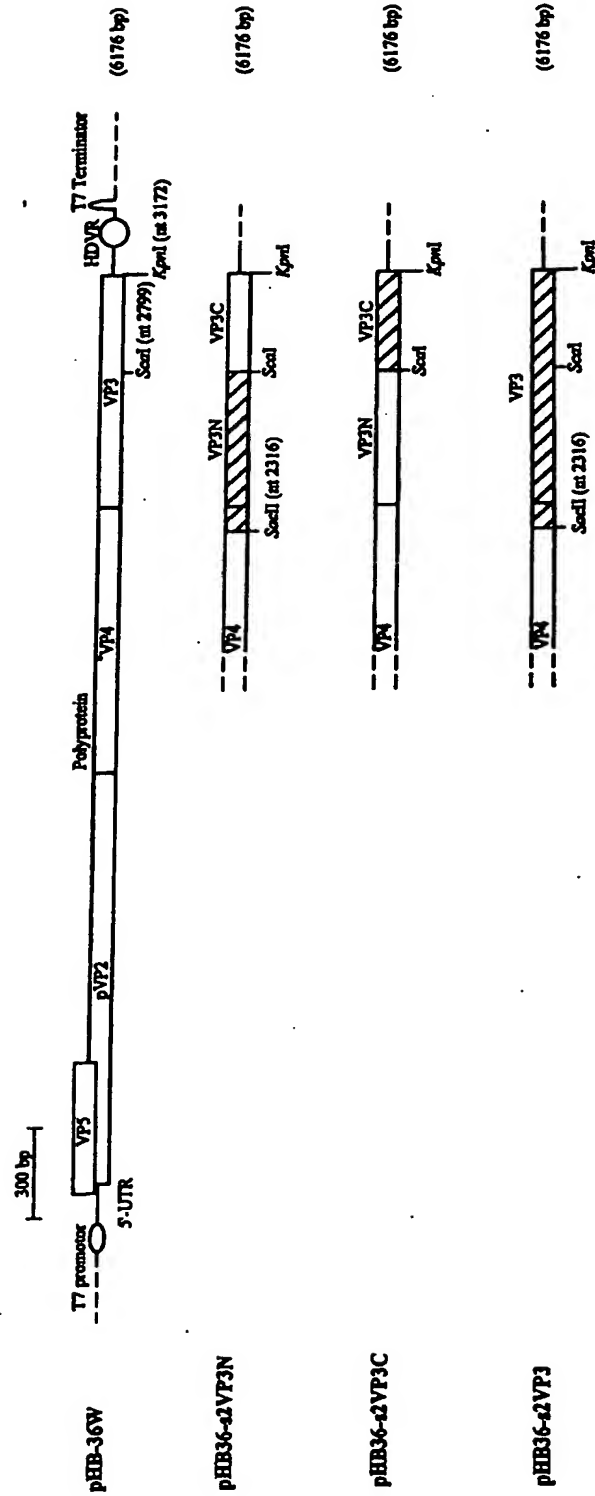


Fig. 7

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Fig. 8C

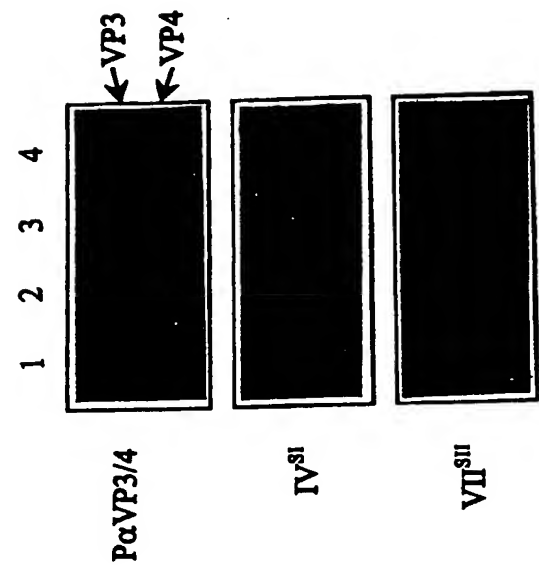


Fig. 8B

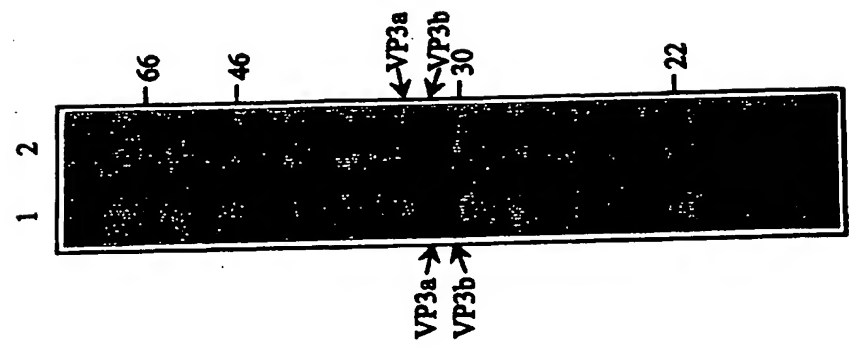
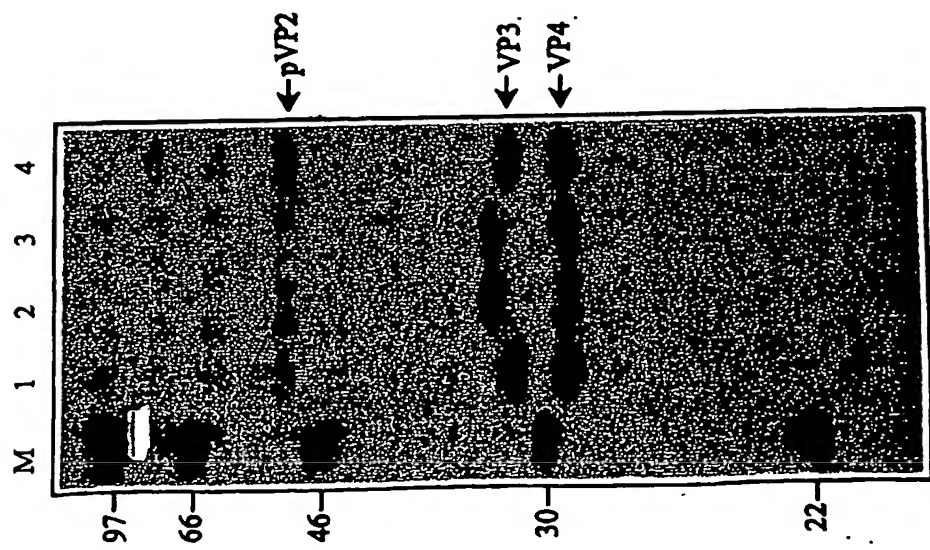


Fig. 8A



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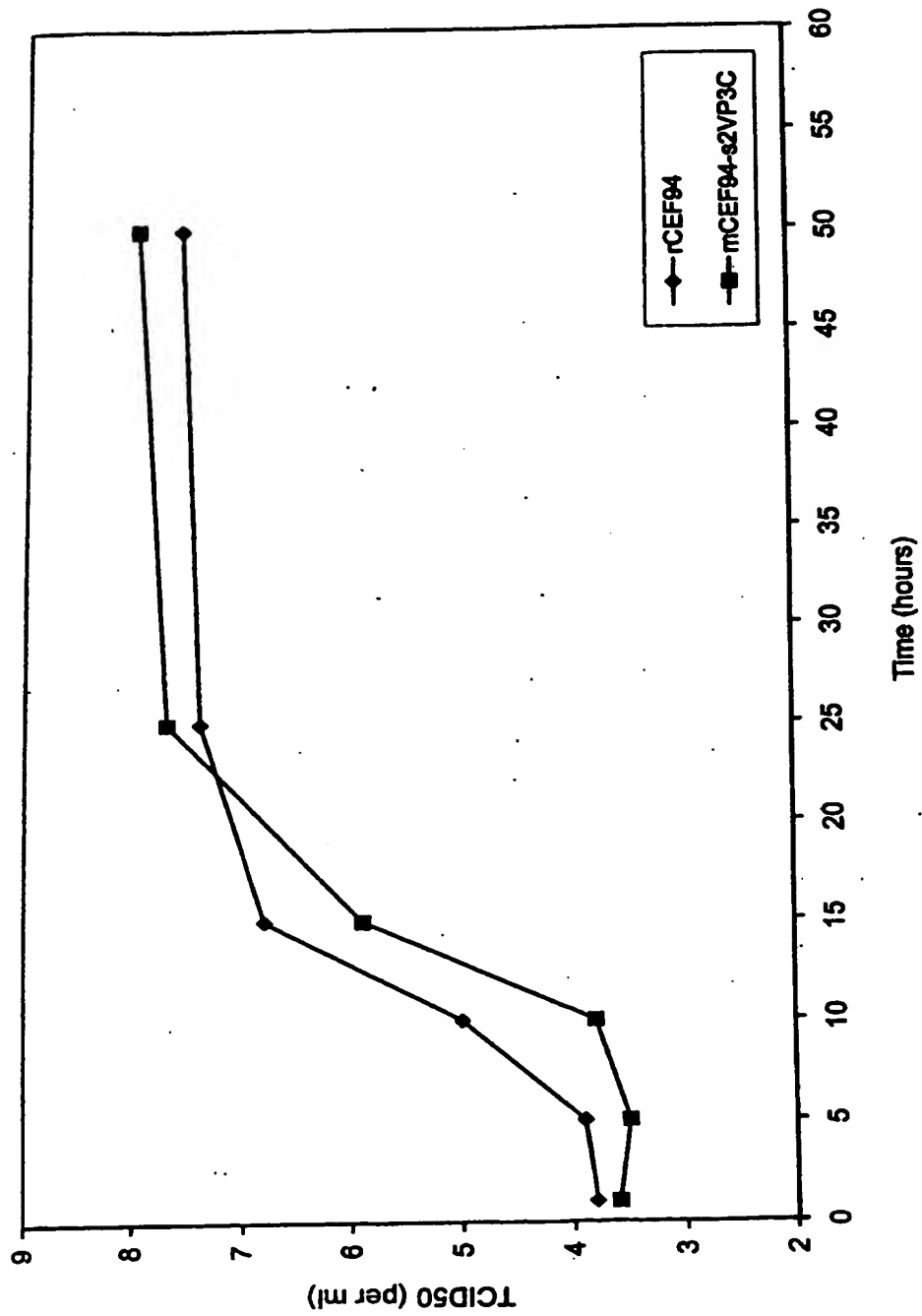


Fig. 9

TITLE: MOSAIC INFECTIOUS BURSAL
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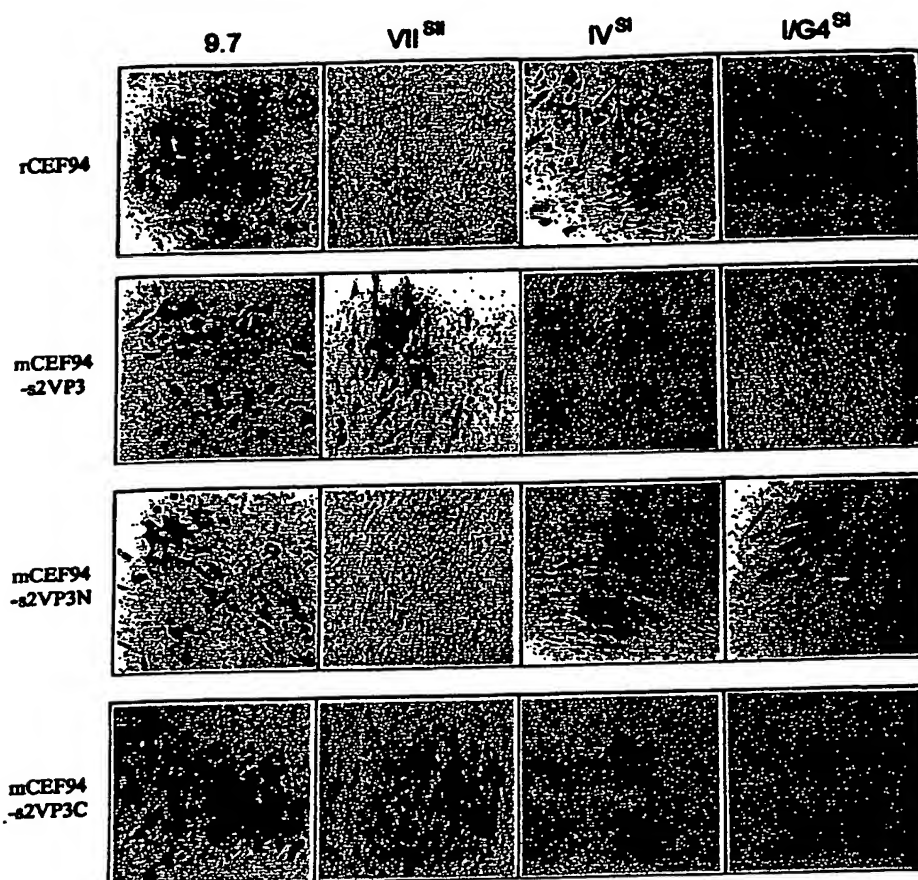
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Fig. 10



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Schematic representation of plasmids pHB60-s2VP3C1 and pHB60-s2VP3C3

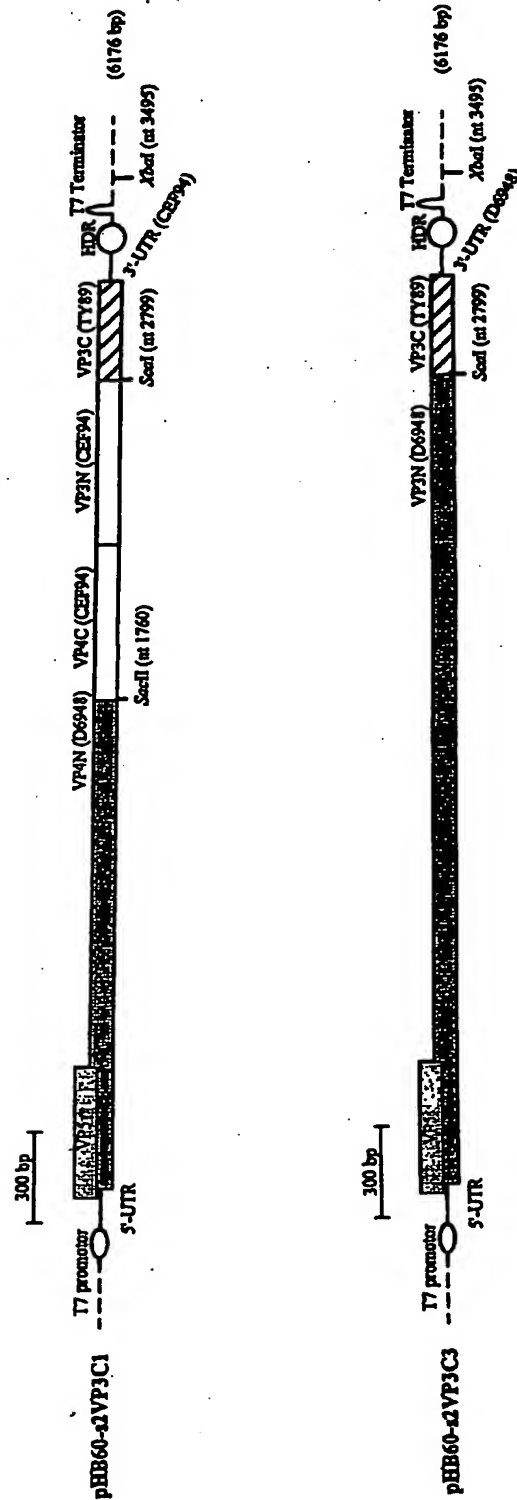


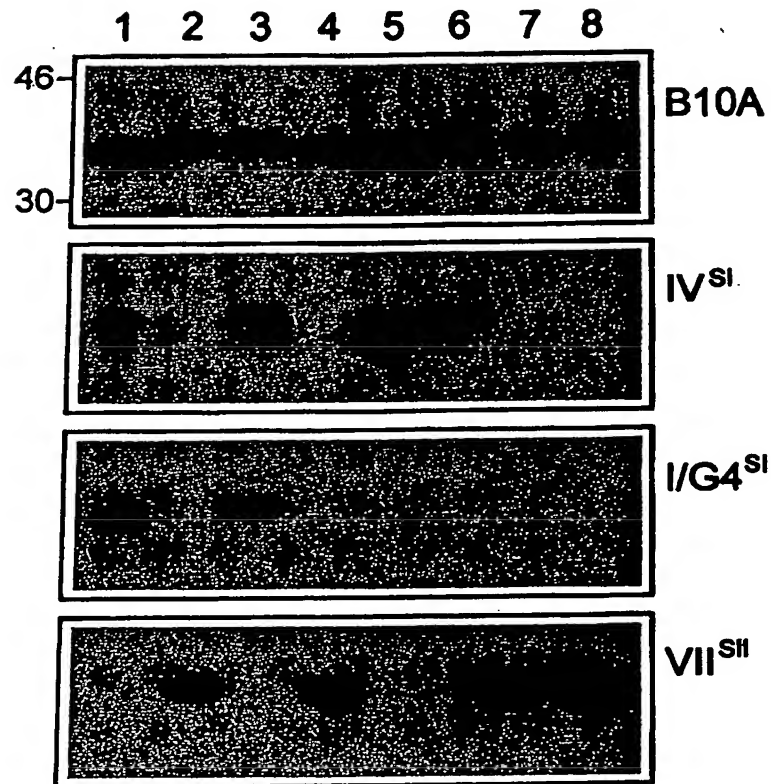
Fig. 11

TITLE: MOSAIC INFECTIOUS BURSAL DISEASE VIRUS VACCINES

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Fig. 12



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Fig. 13

			VP4 ← —→ VP3	
	SecII			
CEF94-PP	724-PPHNPRD	WDRLPYLNL	P	724-PPHNPRD
D6948	724-PPHNPRD	WDRLPYLNL	P	724-PPHNPRD
TY89-PP	724-PPHNPRD	WDRLPYLNL	P	724-PPHNPRD
	SecI			
CEF94-PP	MANFALS	SDPN	AKYGTAGYGV	MANFALS
D6948	MANFALS	SDPN	AKYGTAGYGV	MANFALS
TY89-PP	MANFALS	SDPN	AKYGTAGYGV	MANFALS
CEF94-PP	RGSPGQLKY	WONTREIPDP	NEDYLDYVHA	RGSPGQLKY
D6948	RGSPGQLKY	WONTREIPDP	NEDYLDYVHA	RGSPGQLKY
TY89-PP	RGSPGQLKY	WONTREIPDP	NEDYLDYVHA	RGSPGQLKY
CEF94-PP	QMKOLLITAM	EMKHNPRRA	LPKPKPKPNA	QMKOLLITAM
D6948	QMKOLLITAM	EMKHNPRRA	LPKPKPKPNA	QMKOLLITAM
TY89-PP	QMKOLLITAM	EMKHNPRRA	LPKPKPKPNA	QMKOLLITAM

Fig. 14

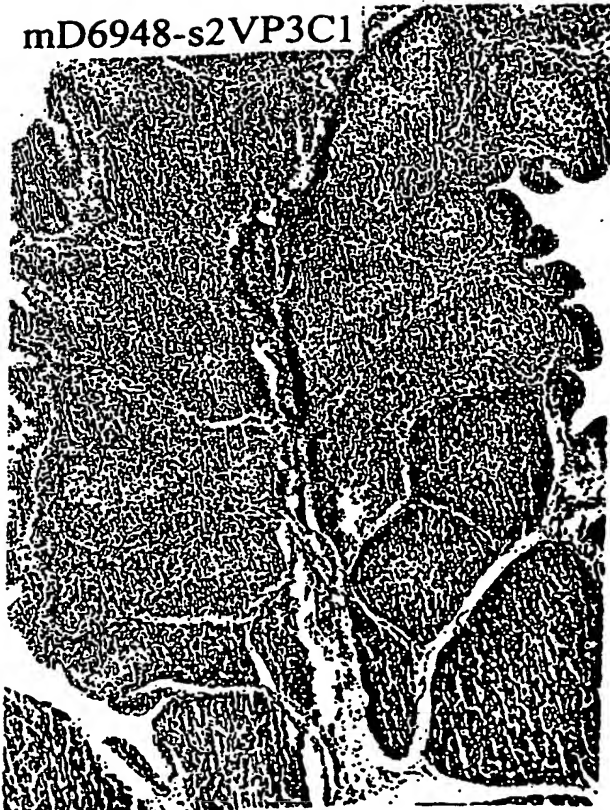
Mock



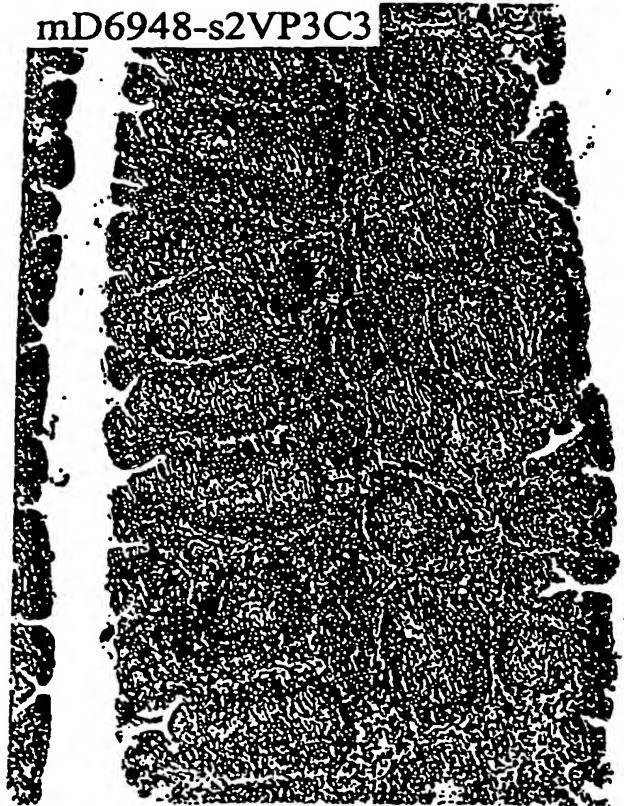
D6948



mD6948-s2VP3C1



mD6948-s2VP3C3



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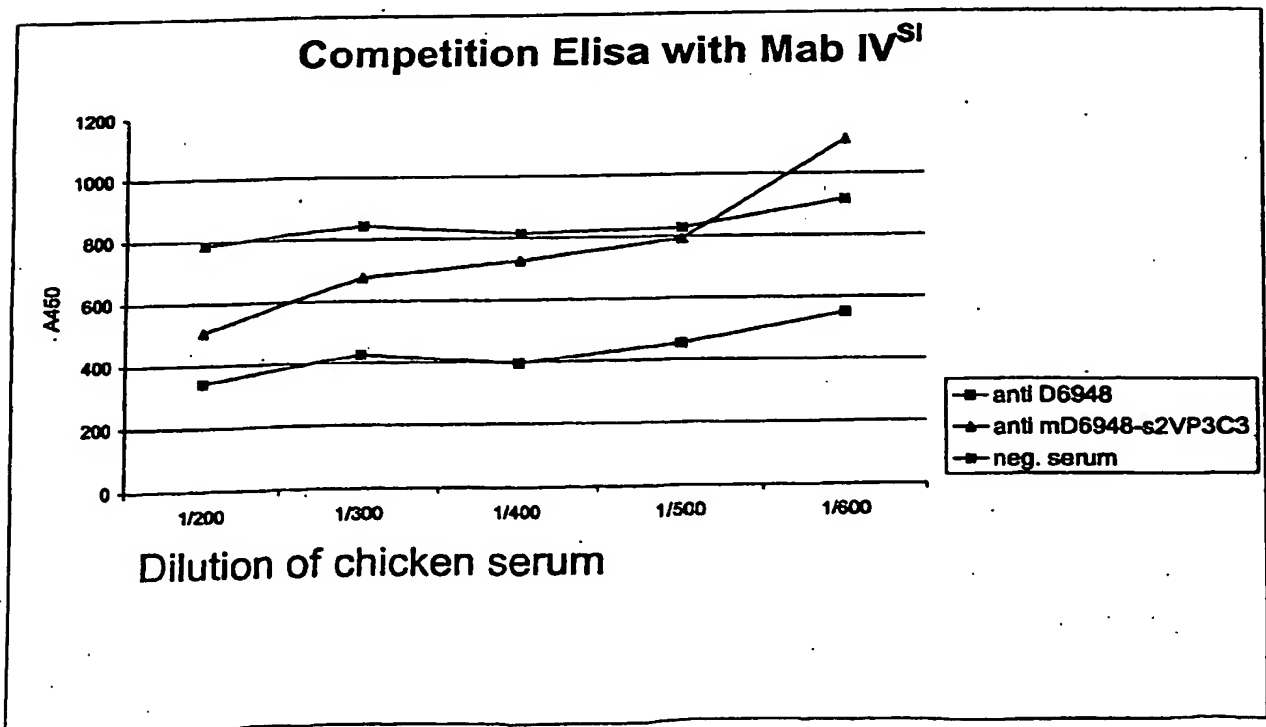
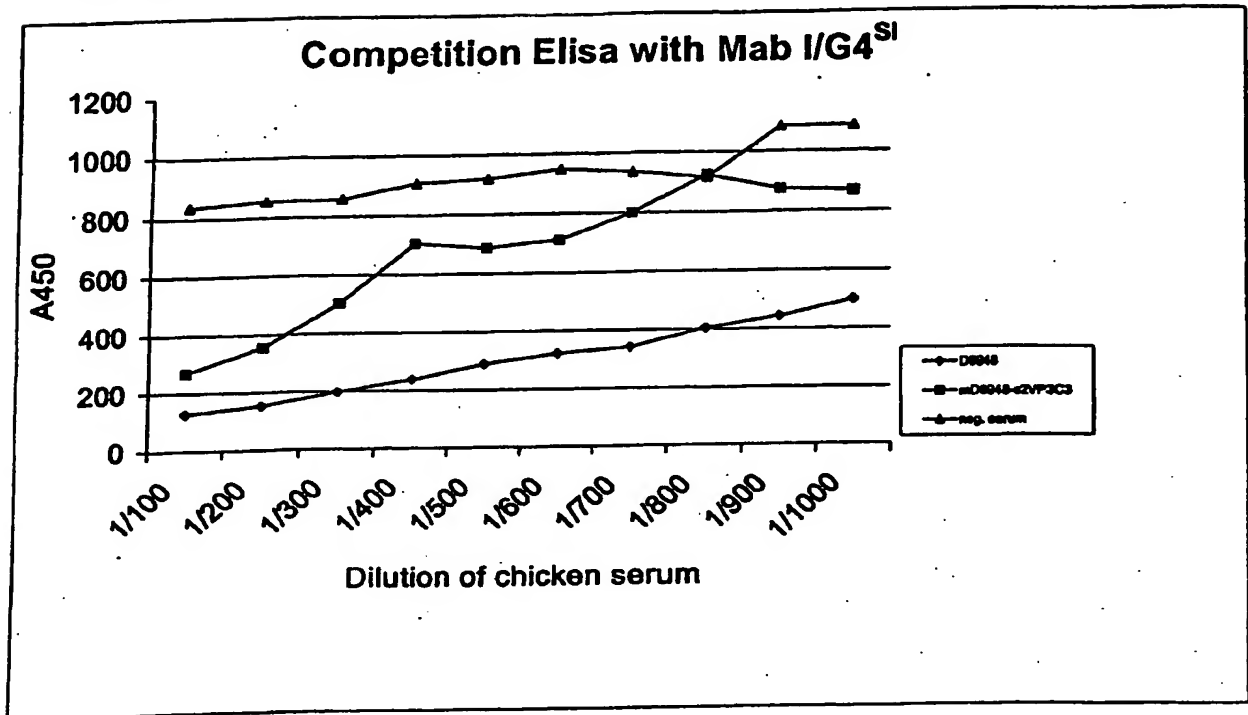
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FIG. 15



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Fig. 16A

D6948-VP5	MLSLMVSBDQ	TNDRSDDEPA	RSNPTDCSVH	TEPSDANNRT	GVHSGRRHPR	AHSQVRDLDL	QFTCGGHRVR	ANCLF	75
CEF94-VP5	-----	K			G				71
	PWPPWLNCGC	SLHTAEQNEL	QVRSDAPDCP	EPTGQLQLLQ	ASESESHSEV	KHTPWRLCT	KNEHKRRDLP	RKPE	149
	I			S		R			145

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Fig. 16B

D6948-PP MTNLQDQTOQ IVVFIRSLM PTTOPASIPD DTLEKHTLRS ETSTYNLTVG DTGSLIVFF PGFPGSIVGA HYTLQ 75
 CEF94-PP SNGNYKFDQM LLTAQNLPAS YNYCRLVRS LTVSSTLPG GYVALNGTIN AVTFQGSLSLSE LTDVSINGLM SATAN 150
 INDKIGNVLV QEGVTVLSP TSYDLGYVRL GDPIPAIGLD PKMVATCDSS DRPRVYTITA ADDYQFSSQY QAGGV 225
 TITLFSANID AITSLSIGGE LVFQTSVQGL ILGATYILIG FDGTAVITRA VAADNGLTAG TDNLMPFNIV IPTSE 300
 ITQPIITSIKL EIVTSKSGGQ AGDOMSWSAS GSLAVTINGG NYPCALRPVT LVAYERVATO SVVTVAGVSN FELIP 375
 NPFLAKNLVT EYGRFDPQAM NYTKLILSER DRLGINKTWP TREYTDREY FMEVADINSP LKLAGAFGEK DIIRA 450
 LRRIAVPEVVS TLFPFAAPLA HAIGEGVDYL LGDEAORASG TARRASGKAR AASGRIROLT LAADKGYEVV ANLEQ 525
 YPONPVVDGI LASPGILGGA HNLDGVLRG ATLEPPVVT VEDANTPKAL NEKMEAVIEG VREDLOPPSO RGSFI 600
 RTLGSHRVYG YAPDGVLPDL TGRDYTVVPI DDVDDDSIML SKDPIPIVG NSGNLAAYM DVEPKVPIH VAMTG 675
 ALNAYGBIEN VSKRSTKLAT AHRIGLKLAG PGAFDVNTGS NMAFLAKRFP HNPRDWRDLP YMLPYLPPN AGROY 750
 DLAMAASEFK ETPELESVR AMEAAANVDP LFQSALSVM WLEENGIVTD MANFALSDEPN AHRMRNFLAN APQAG 825
 SKSQRAKYGT AGYGVZARGP TPFAQREKD TRISKMETM GIYFATPEWV ALNGHROPSP GOLKIWNTR EIPDP 900
 NEDYLDYVHA EKSRLASEQ ILRAATSIYG APQAEPPQA FIDEVAKVE INHGRGPQOE QMKDILLTAM EMKHR 975
 NRRAPPKPK PKPNAPTQRP PGLGRWIRA VSEDELE 1012
 L T

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Fig. 16C

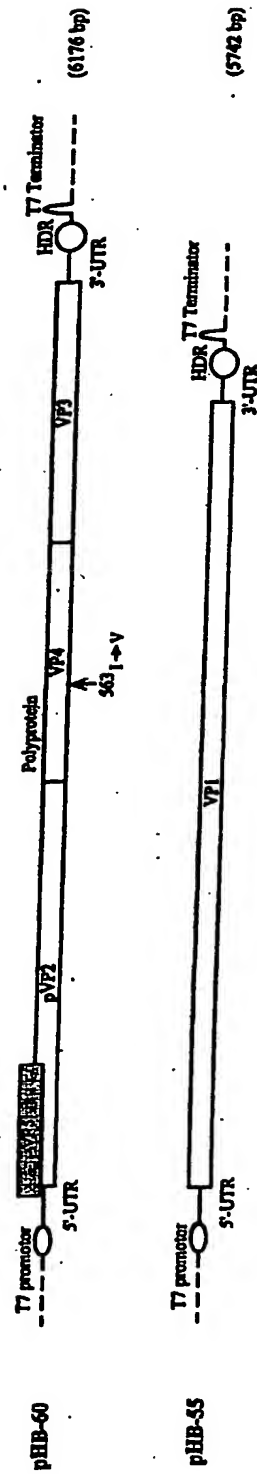
D6948-VP1		I T	MSDVFNSPQA RSKISAAFGI KPTAGQDVEE LLIPKVVWPP EDPLASPSRL AKFLRENGYK ILQPRSLPEN BEYET V	75
CEP94-VP1		T	DQILPDLAWM QRIEGAVLKP TLSLPICGQE YPKKYYPTHR PSKEKNPAYP PDIALLKQMI YLFLOVPEAT DNLD N EQ	150
			EVTLLTONIR DKAYSGTYM GQATRLVANR EVATORNPVK DPLKLGYTFB SIAQLDLITL PVGPPEGDDX PNVPL	225
		D	TRVPSRMVLV TGDVDGEFEV EDYLPKINLK SSSGLPYVR TRGETIGEMI AISNOFLREL SALLAQCACT KGSNK T	300
		L Z	KKLSMLSDY WYLSCOLLFP KAERYDKSTM LTKTRNWSA PSPHLMISM ITWFVNNSNP NNVLNIQGCP SLIKF	375
		Z	NPFRRGLNR I VEWIMAPDEP KALVYADNY IVHSNTWYSI DLERGEANCT RHMQAMWY ILTRGWSDNG DPMPN	450
		R	QTWATTAMNI APALVVDSSC LIMNLQIKTY GGSGNAATF INNHLLSTLY LDQMNLAKQP SPDSEEFKS I HDKLG R	525
		S	INFKIERSID DIRGLEROLV PLAQQOYLSG OVEPEQBSPFT VELDLLGWSA TYSKDILGIYV PYLDKERLFC SAAYP	600
		G	KOVENKSLKS KVGBIOAYKV VRYEALRLVG GWNYPLANKA CKNNABAARR HLEAKGPPLED EFLEAWSBELS BFOEA	675
		X	PBGFINIKLV TPESLAELENR FVPPKKPNVN RPVNTGGJKA VSNALKTGRY RNHEAGLSGLV LLATARSRLO DAUKA	750
		B	KABAEKLHK KSDDDPAOWF ERSETLSDDL EKADIASKVA HSALVETSDA LEAVOSTSVY TPPYPEVKNP QTASN	825
		--	FVVGLHLPAK RATGVQAALL GAGTSRPMM EPATRSKNV KWAKRRQRK ESRO-- OP	879
				881

TITLE: MOSAIC INFECTIOUS BURSA
DISEASE VIRUS VACCINES

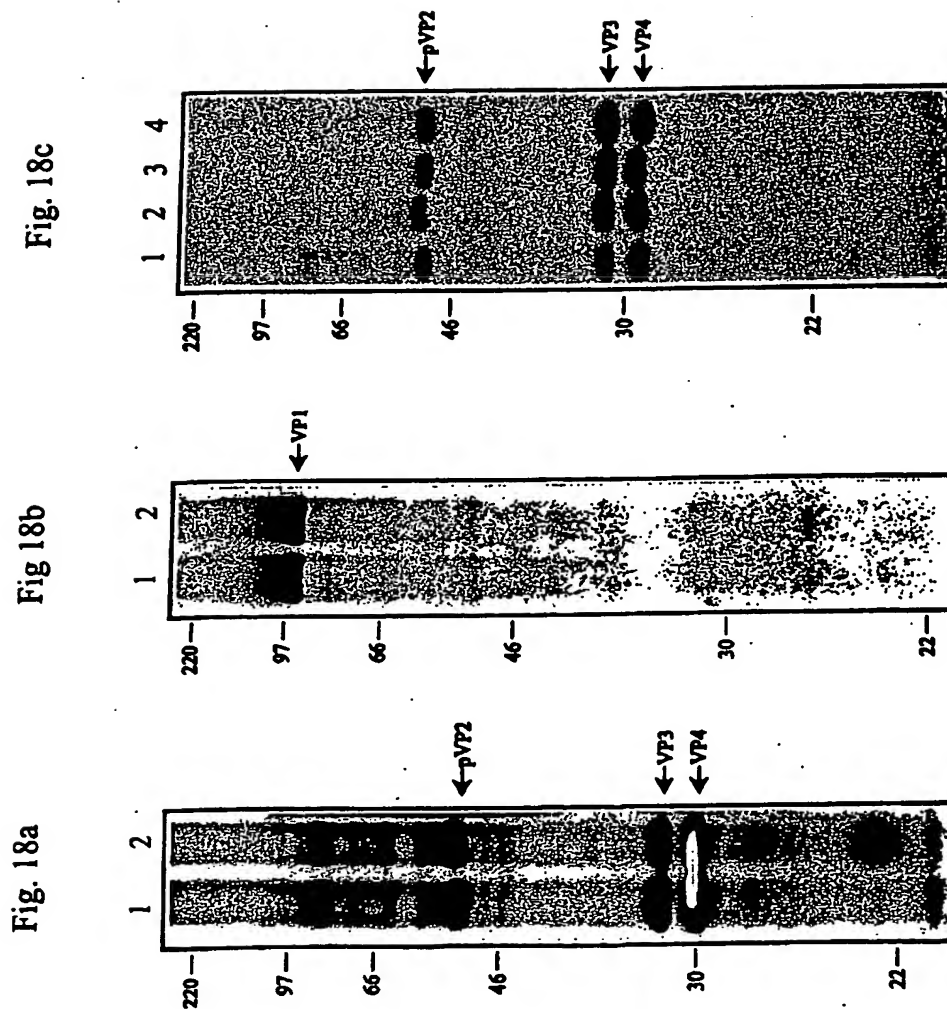
Inventor: Boot et al.
Serial No.: 10/046,671
Docket No.: 2183-5238US

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Fig. 17



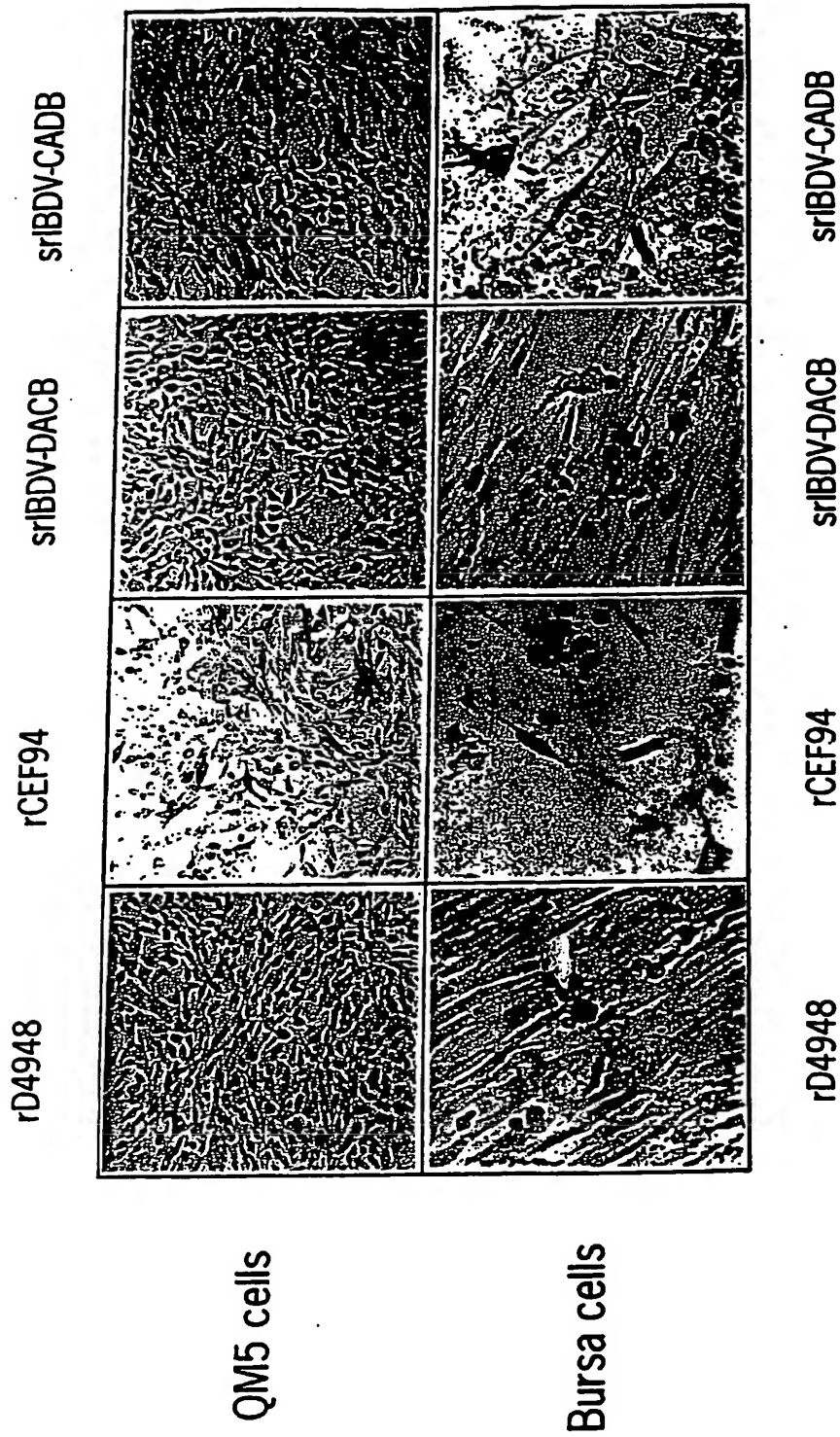
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TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINESInventor: Boot et al.
Serial No.: 10/046,671
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Fig. 19



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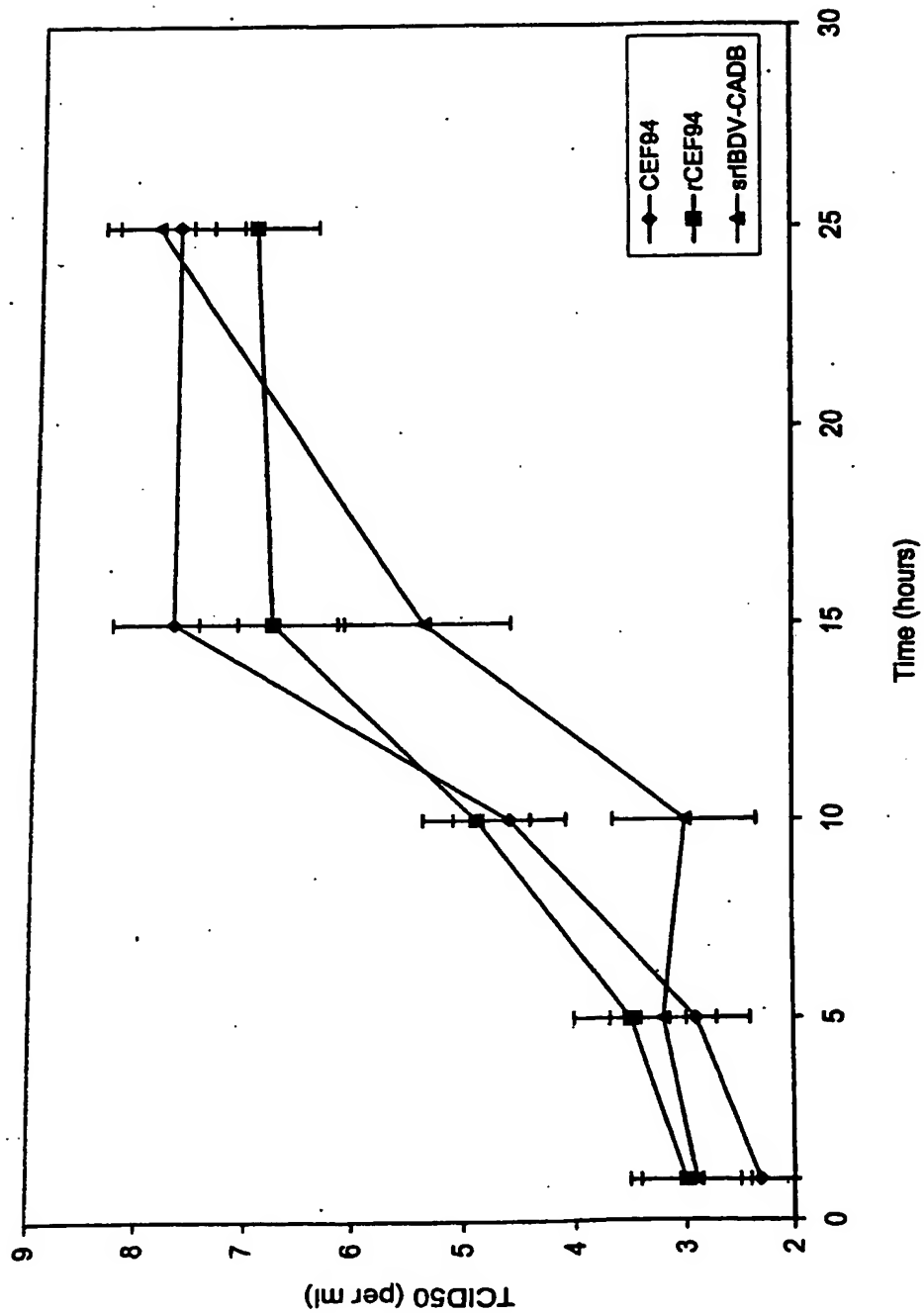
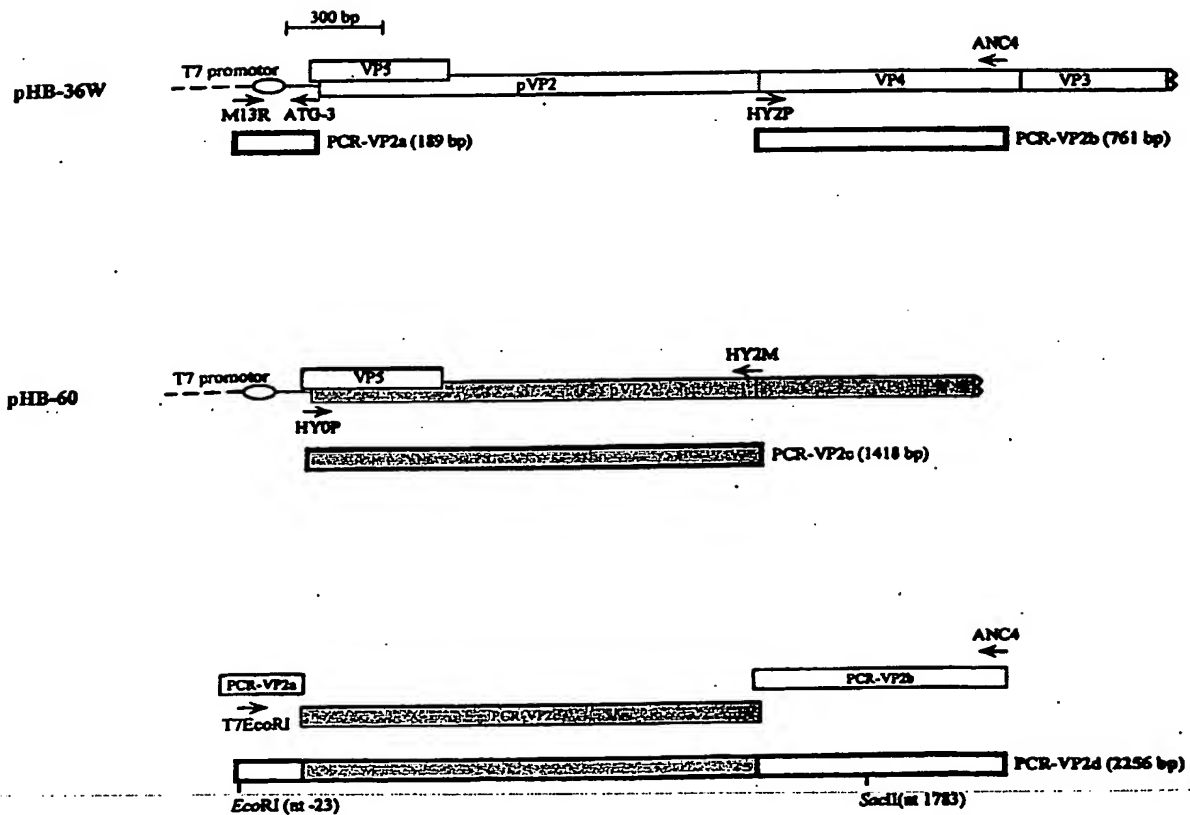


Fig. 20

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Fig. 21



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Fig. 22

